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OM protein - protein search, using sw model

Run on: June 1, 2004, 17:58:38 ; Search time 55 Seconds

(without alignments)
30.823 Million cell updates/sec

Title: US-09-715-763A-5

Perfect score: 34

Sequence: 1 DGDGFA 6

Scoring table: BL05M62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: GeneseqP1980s:*

2: GeneseqP1990s:*

3: GeneseqP2000s:*

4: GeneseqP2001s:*

5: GeneseqP2002s:*

6: GeneseqP2003as:*

7: GeneseqP2003bs:*

8: GeneseqP2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	34	100.0	6	4	Aae07240		Aae07240 Peptide #
2	34	100.0	218	2	AAW89832		Aaw89832 Protein e
3	34	100.0	256	6	ABP79797		Abp79797 N. gonorr
4	34	100.0	273	2	AAW90026		Aaw90026 Expressed
5	34	100.0	273	2	AAW89979		Aaw89979 Protein e
6	34	100.0	274	2	AAW19756		Aaw19756 2-Oxogl
7	34	100.0	326	6	ABU15067		Abu15067 Protein e
8	31	91.2	14	2	AAW90308		Aaw90308 Human ant
9	31	91.2	122	2	AAW90284		Aaw90284 Human ant
10	31	91.2	210	4	AGB3113		Aag3113 S. epider
11	31	91.2	210	4	AGB82885		Aag82885 S. epider
12	31	91.2	288	5	ABP40124		Abp40124 Staphyloc
13	31	91.2	288	6	ABU7102		Abu7102 Staphyloc
14	31	91.2	763	6	ABU20715		Abu20715 Protein e
15	31	91.2	796	4	AGT0833		Aag70833 C albican
16	31	91.2	921	2	AY34522		Aay34522 Porphyrin
17	31	91.2	922	2	AY34521		Aay34521 Porphyrin
18	31	91.2	925	2	AY34520		Aay4520 Porphyrin
19	31	91.2	938	2	AY34392		Aay34392 Porphyrin
20	30	88.2	53	4	AM13393		Aam13393 Peptide #
21	30	88.2	53	4	ABP37424		Abp37424 Peptide #
22	30	88.2	53	4	ABP32184		Abp32184 Peptide #
23	30	88.2	53	4	ABP22127		Abp22127 Protein #
24	30	88.2	63	5	ABP31235		Abp31235 Human ORF
25	30	88.2	78	2	AY25642		Aay25642 Phleum sp

26	30	88.2	78	7	ADC34891	Timothy g
27	30	88.2	81	7	ADC94212	E. faeciu
28	30	88.2	83	3	AAG19054	Zea mays
29	30	88.2	85	2	AAV25652	Berula sp
30	30	88.2	85	7	ADC34901	Tree alle
31	30	88.2	88	3	AAG06095	Arabidops
32	30	88.2	91	3	AAG44004	Zea mays
33	30	88.2	92	4	AAM43531	Human pol
34	30	88.2	92	4	AUJ19932	Novel hum
35	30	88.2	92	4	Au87507	Novel cen
36	30	88.2	92	4	AAU87196	Novel cen
37	30	88.2	102	4	AAU52864	Propionib
38	30	88.2	102	6	ABN49383	Propionib
39	30	88.2	122	7	ADC96103	E. faeciu
40	30	88.2	128	3	AAG19053	Zea mays
41	30	88.2	129	3	AGA48315	Arabidops
42	30	88.2	129	3	AAG04159	Arabidops
43	30	88.2	136	3	AAG44003	Zea mays
44	30	88.2	140	2	AAR27559	Cyn d all
45	30	88.2	143	2	AAR27560	Cyn d all

ALIGNMENTS

RESULT 1							
ID	AAE07240						
AC	AAE07240;						
DT	06-NOV-2001						
DE	Peptide #5 used for counteracting effects of ROS and free radicals.						
XX	Antioxidative enzyme; catalase; CAT; superoxide dismutase; SOD; therapy; reactive oxygen species; ROS; free radical; dietary supplement; stroke; AP-1 transcription factor; renal reperfusion damage; cerebral ischaemia; myocardial infarction; heart attack; pain; atherosclerosis; tardive dyskinesia; trauma; premature aging; neurodegenerative disease; Parkinson's disease; arthritis; inflammatory disease; diabetes; ulcerative colitis; cataract; sensitivity; Down's syndrome; macular degeneration; septic shock; epilepsy; polytraumatic shock; schizophrenia; antiulcer; clozapine; tranquiliser; carisain; cerebroprotective; vulnary; nootropic; Huntington's disease; cytotoxic; neuroprotective; antiarthritic; antiinflammatory; burn; immunosuppressive.						
OS	Synthetic.						
XX							
Key							
Modified-site							
FT	1 note = "Optionally protected with glucose-3-O-glycolic acid moiety, palmitoyl group or lipoic acid"						
XX	WO200136454-A1.						
PD	25-MAY-2001.						
XX							
PT	17-NOV-2000; 2000WO-US031764.						
XX							
PR	18-NOV-1999; 99US-0166381P.						
XX							
PA	(CERE-) CEREMEDIX INC.						
XX							
PI	Shashoua VE;						
XX							
DR	WPI; 2001-496512/54.						
XX							
PT	Novel peptide compound that up regulates expression of a gene encoding antioxidant enzymes, used to treat or prevent conditions caused by undesirable elevation of reactive oxygen species and other free radicals.						
PT							

XX Claim 4; Page 63; 102pp; English.

XX The invention relates to peptide compounds and methods for upregulating expression of a gene encoding an antioxidant enzyme, such as catalase (CAT) or superoxide dismutase (SOD), to counteract harmful oxidative effects of reactive oxygen species (ROS) and other free radicals. The peptides are used as components of pharmaceuticals and dietary supplements. The peptides are used to treat or to prevent diseases and conditions characterised by undesirable elevation of ROS and other free radicals, to upregulate AP-1 transcription factor gene expression and to treat pain. The disease or conditions include renal reperfusion damage, cerebral ischaemia (stroke), myocardial infarction (heart attack), head trauma, atherosclerosis, brain trauma, oxygen toxicity in premature infants, premature ageing, spinal cord trauma, neurodegenerative diseases, Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis, Alzheimer's disease, arthritis and other inflammatory diseases, diabetes, ulcerative colitis, human leukaemia and other cancers characterised by elevation of ROS or free radicals, age-related elevation of ROS or free radicals, senility, Down's syndrome, macular degeneration, cataracts, epileptic shock, polytraumatic shock, schizophrenia, burn injuries, CC radicals, where the drug is a neuroleptic or a drug such as clozapine defined in the specification and Tardive dyskinesia. The present sequence XX is a peptide used for counteracting effects of ROS and free radicals.

Sequence 6 AA;

Query Match Score 34; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DGDGFA 6
Db 1 DGDGFA 6

RESULT 2
ID AAW899832
AAW89832 standard; protein; 218 AA.

XX AAW89832;

XX 20-MAR-2003 (revised)
DT 18-FEB-1999 (first entry)

DE Protein encoded by clone a3 ORF2.

XX Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis;
KW peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
OS Helicobacter pylori.

XX WO9849314-A2.

XX 05-NOV-1998.

XX PF 25-APR-1998; 98WO-US008487.

XX PR 25-APR-1997; 97US-0045107P.

PR 14-OCT-1997; 97US-006158P.

XX (GENE-) GENELABS TECHNOLOGIES INC.

XX PI Chow TP, FRY KE, Lim MY, McAtee CP;

XX DR WPI: 1999-009413/01.

XX DR N-PSDB; AAV90766.

XX New Helicobacter pylori antigens and related nucleic acid sequences -
PT useful in serological diagnosis and protective vaccines, providing long-
lasting immune response.

XX PT Sequence 256 AA;

Query Match Score 34; DB 6; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;

PS Claim 15; Page 178; 402pp; English.

XX The present sequence represents a *Helicobacter pylori* antigenic protein CC that is characterised by immunoreactivity with *H. pylori* antisera. The proteins are highly immunogenic and induce a long-lasting CC immune response that persists even after antimicrobial treatment. In CC antibody-detection assays, on sera, plasma, urine, saliva etc., they are CC highly sensitive and specific. The specification also describes 69 CC previously unrecognised immunogenic cluster families. *H. pylori* antigens CC are used to detect *H. pylori*-specific antibodies, for diagnosing CC infection or to confirm eradication of infection, and in vaccines to CC protect against *H. pylori* infection and related diseases (gastritis, CC peptic ulcer, gastric adenocarcinoma/lymphoma). (Updated on 20-MAR-2003 CC to correct PPI field.)

XX Sequence 218 AA;

SQ Query Match Score 34; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DGDGFA 6
Db 95 DGDGFA 100

RESULT 3

ABP79797
ID ABP79797 standard; protein; 256 AA.
XX ABP79797;
AC ABP79797;
DT 07-MAR-2003 (first entry)
XX N. gonorrhoeae amino acid sequence SEQ ID 6124.
XX DE Antibacterial; infection; vaccine; gene therapy.
XX KW Neisseria gonorrhoeae.
XX OS Neisseria gonorrhoeae.
XX WO200279243-A2.
PN PN
XX 10-OCT-2002.
PD PD
XX 12-FEB-2002; 2002WO-IB002069.
PP PR
XX 12-FEB-2001; 2001GB-00003424.
PA PA (CHIRON SPA.
XX PI Fontana MR, Pizza M, Massignani V, Monaci E;
XX DR WPI: 2003-058415/05.
DR N-PSDB; ABZ40767.

XX New protein from *Neisseria gonorrhoeae*, useful for the manufacture of a CC medicament for treating or preventing *N. gonorrhoeae* infection.
PT
XX Disclosure; Page 635; 815pp; English.
PS
XX The present invention relates to proteins from *Neisseria gonorrhoeae*.
CC Also disclosed are the nucleic acid molecules encoding the proteins and
CC antibodies that specifically bind to the proteins. The composition
CC comprising the protein, nucleic acid or antibody is useful for the
CC manufacture of a medicament for treating or preventing *N. gonorrhoeae*
CC infection, this may be in the form of a vaccine or gene therapy.
CC Sequences given in records ABP76736-ABP81046 represent nucleic acid
CC molecules of the invention
XX SQ Sequence 256 AA;

Query Match Score 34; DB 6; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches	Conservative	Mismatches	Indels	Gaps	0;		XX	DT 20-MAR-2003 (revised)
Qy	1 DGDGFA 6 	0;	0;	0;			XX	DT 18-FEB-1999 (first entry)
Db	49 DGDGFA 54						XX	Protein encoded by clone d11 ORF2.
							XX	KW Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
RESULT 4							XX	KW Peptic ulcer; Helicobacter pylori.
ID AAW90026	AAW90026 standard; protein; 273 AA.						OS	
XX							XX	
AC AAW90026;							PN WO9849314-A2.	
XX							XX	
DT 20-MAR-2003 (revised)							PD 05-NOV-1998.	
DT 18-FEB-1999 (first entry)							PF 25-APR-1998; 98WO-US008487.	
DE Expressed antigen for cluster 50.							XX	
XX							PR 25-APR-1997; 97US-0045107P.	
KW Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.							PR 14-OCT-1997; 97US-0061958P.	
XX							XX	
XX							PA (GENE-) GENELABS TECHNOLOGIES INC.	
OS Helicobacter pylori.							XX	
XX							PI Chow TP, Fry KE, Lim MY, Mcatee CP;	
PN WO9849314-A2.							XX	
XX							DR WPI: 1999-009433/01.	
PD 05-NOV-1998.							XX	
XX							DR N-PSDB; AAV90921.	
PF 25-APR-1998; 98WO-US008487.							XX	
XX							PT New Helicobacter pylori antigens and related nucleic acid sequences -	
PR 25-APR-1997; 97US-0045107P.							PT useful in serological diagnosis and protective vaccines, providing long-	
PR 14-OCT-1997; 97US-0061958P.							PT lasting immune response.	
XX							XX	
PA (GENE-) GENELABS TECHNOLOGIES INC.							PS Claim 15; Page 319; 402pp; English.	
XX							XX	
XX							CC The present sequence represents a Helicobacter pylori antigenic protein	
PI Chow TP, Fry KE, Lim MY, Mcatee CP;							CC that is characterised by immunoreactivity with H. pylori-positive	
XX							CC antisera. The proteins are highly immunogenic and induce a long-lasting	
DR WPI: 1999-009433/01.							CC immune response that persists even after antimicrobial treatment. In	
XX							CC antibody-detection assays, on sera, plasma, urine, saliva etc., they are	
PT New Helicobacter pylori antigens and related nucleic acid sequences -							CC highly sensitive and specific. The specification also describes 69	
XX							CC previously unrecognised immunogenic cluster families. H. pylori antigens	
PT useful in serological diagnosis and protective vaccines, providing long-							CC are used to detect H. pylori-specific antibodies, for diagnosing	
PT lasting immune response.							CC infection or to confirm eradication of infection, and in vaccines to	
XX							CC protect against H. pylori infection and related diseases (gastritis,	
PS Claim 16; Page 347-348; 402pp; English.							CC peptic ulcer, gastric adenocarcinoma/lymphoma). (Updated on 20-MAR-2003	
XX							CC to correct PF field.)	
CC The present sequence represents a Helicobacter pylori antigenic protein							XX	
CC that is characterised by immunoreactivity with H. pylori-positive							SQ Sequence 273 AA;	
CC antisera. The proteins are highly immunogenic and induce a long-lasting							Query Match 100.0%; Score 34; DB 2; Length 273;	
CC immune response that persists even after antimicrobial treatment. In							Best Local Similarity 100.0%; Pred. No. 1.5e+02;	
CC antibody-detection assays, on sera, plasma, urine, saliva etc., they are							Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
CC highly sensitive and specific. The specification also describes 69							XX	
CC previously unrecognised immunogenic cluster families. H. pylori antigens							AC AAW19756;	
CC are used to detect H. pylori-specific antibodies, for diagnosing							XX	
CC infection or to confirm eradication of infection, and in vaccines to							DT 17-SEP-1997 (first entry)	
CC protect against H. pylori infection and related diseases (gastritis,							XX	
CC peptic ulcer, gastric adenocarcinoma/lymphoma). (Updated on 20-MAR-2003							DB 2-Oxoglutarate:acceptor oxidoreductase subunit (ORF3 product).	
XX							XX	
XX							AC AAW89979;	
PS Sequence 273 AA;							XX	
Query Match 100.0%; Score 34; DB 2; Length 273;							AC AAW89975	
Best Local Similarity 100.0%; Pred. No. 1.5e+02;							ID AAW19756 standard; protein; 274 AA.	
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							XX	
Qy 1 DGDGFA 6 							XX	
Db 95 DGDGFA 100							DB 2-Oxoglutarate:acceptor oxidoreductase subunit (ORF3 product).	
							XX	
RESULT 5							AC AAW89979;	
AAW89979 ID AAW89979 standard; protein; 273 AA.							XX	
XX AC AAW89979;							PN WO9723526-A1.	

PD 03-JUL-1997.
 XX WPI; 2003-029926/02.
 PF 17-DEC-1996; 96WO-GB003119.
 XX N-PSDB; ACR18937.
 PR 22-DEC-1995; 95GB-00026407.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PT Chalk PA, Clayton CL, Kelly DJ, Hughes NJ;
 XX WPI; 1997-351063/32.
 DR N-PSDB; AAT72718.
 XX
 PT New isolated Helicobacter pylori oido:reductase enzymes - used to develop products for the diagnosis, treatment and prevention of H. pylori mediated diseases or disorders.
 XX
 PS Example A; Fig 1; 36pp; English.
 XX
 CC 4 Polypeptides (AAW19754-57) comprise the subunits of a newly identified tetrameric 2-oxoglutarate:acceptor oxidoreductase (OAO) of Helicobacter pylori. Their amino acid sequences were deduced from the open reading frames of a single operon (AAT72718) isolated from a cosmid library. The ORF3 product has a predicted mol.wt. of 30.6 kDa and shows sequence similarity to Halobacterium halobium small pyruvate oxidoreductase. The OAO subunit polypeptides can be expressed in transformed host cells. OAO and a newly identified pyruvate:ferredoxin oxidoreductase (see also AAW19758-61) are important or essential to H. pylori but are not expressed by humans and can therefore be used in vaccines or to screen for agents that can be used to treat H. pylori diseases or disorders.
 XX Sequence 274 AA;
 CC 100.0%; Score 34; DB 2; Length 274;
 CC Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 Qy 1 DGDGFA 6
 Db 95 DGDGFA 100
 XX SQ Sequence 326 AA;
 CC Query Match 100.0%; Score 34; DB 6;
 CC Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 RESULT 7
 ABU15067 ABU15067 standard; protein; 326 AA.
 ID ID AAW90308 standard; protein; 14 AA.
 AC AC
 ABU15067;
 XX DT 07-SEP-1999 (first entry)
 XX DE Protein encoded by Prokaryotic essential gene #594.
 XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX OS Escherichia coli.
 XX PN WO200277183-A2.
 XX
 XX PD 03-OCT-2002.
 XX DE Human anti-idiotype antibody heavy chain protein CDR3 region 4.
 XX PR 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948992.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX PN WO955619-A1.
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Olsens KL, Zyskind JW,
 PI Wall D, Trawick JD, Carr GD, Yamamoto R, Forsyth RA,
 XX
 DR WPI; 2003-029926/02.
 XX PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
 XX PT
 XX PS Claim 25; SEQ ID NO 42991; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of the 5213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct Sequences
 XX SQ Sequence 326 AA;
 CC Query Match 100.0%; Score 34; DB 6;
 CC Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 RESULT 8
 AAW90308 AAW90308 standard; protein; 14 AA.
 ID ID AAW90308;
 AC AC
 XX DT 07-SEP-1999 (first entry)
 XX DE Human anti-idiotype antibody heavy chain protein CDR3 region 4.
 XX PR 1 DGDGFA 6
 DB 78 DGDGFA 83
 OS Homo sapiens.
 XX
 RESULT 9
 AAW90308 AAW90308 standard; protein; 14 AA.
 ID ID AAW90308;
 AC AC
 XX DT 07-SEP-1999 (first entry)
 XX DE Human anti-idiotype antibody heavy chain protein CDR3 region 4.
 XX PR 1 DGDGFA 6
 DB 78 DGDGFA 83
 OS Homo sapiens.

PT polypeptide, useful for diagnosing and treating bacterial infections.
 XX Disclosure; SEQ ID NO 4969; 267pp; English.

PS ABN93378 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP3124 to ABP37965. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site

XX Sequence 288 AA;
 SQ ABM73102 standard; protein; 288 AA.

Query Match 91.2%; Score 31; DB 6; Length 288;
 Best Local Similarity 83.3%; Pred. No. 5.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DGDGFA 6
 Db 92 DGDGYA 97

RESULT 14
 ID ABU20715
 ID ABU20715 standard; protein; 763 AA.
 XX AC ABU20715;
 XX DT 19-JUN-2003 (first entry)
 XX DE Protein encoded by Prokaryotic essential gene #6242.
 XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 OS Bacteroides fragilis.
 XX PN WO200277183-A2.
 XX PD 03-OCT-2002.
 XX PP 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948193.
 PR 25-OCT-2001; 2001US-0342943P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362639P.
 XX EA (ELIT-) ELITRA PHARM INC.
 XX FI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlseni KL, Zyskind JW,
 FI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI; 2003-029926/02.
 XX PR New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 isolate candidate molecules for rational drug discovery programs.
 XX PS Claim 25; SEQ ID NO 48639; 1766pp; English.

XX CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC cellular proliferation or the activity of the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-regulated gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for

XX PI Massignani V, Mora M, Scarselli M;
 XX DR WPI; 2003-120786/11.
 DR N-PSDB; ACF1662.

XX PT New Staphylococcus aureus protein, useful as a vaccine for treating or
 PT preventing Staphylococcal infection, specifically an infection caused by
 PT S. aureus, e.g. sepsis.
 PA (CHIR-) CHIRON SPA.

XX PS Claim 1; SEQ ID NO 4684; 49pp; English.

XX CC The invention relates to novel genes and encoded proteins from
 CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC used as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to Staphylococcus bacteria, specifically an
 CC infection caused by S. aureus. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel S. aureus proteins of the invention

CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences

XX Sequence 763 AA;

Query Match 91.2%; Score 31; DB 6; Length 763;

Best Local Similarity 93.3%; Pred. No. 1.6e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DGDGFA 6
 |||||:
 Db 292 DGDGFS 297

RESULT 15

AAG7083.3

ID AAG7083 standard; protein; 796 AA.

XX AC AAG7083.3;
 XX DT 27-JUL-2001 (first entry)
 XX C albicans apoptosis associated protein #13.

XX DE Yeast; fungus; apoptosis; infection; proliferative disease; vaccine;
 KW autoimmune disease; ischaemia; neurodegeneration.
 XX Candida albicans.
 XX PN WO200102550-A2.

XX PD 11-JAN-2001.
 XX PF 03-JUL-2000; 2000WO-BE0000077.
 XX PR 01-JUL-1999; 99EP-00870141.

XX PA (JANS) JANSSEN PHARM NV.
 XX Contreras RH, De Backer MD, Luyten WHML, Malcorps IKL;
 PI Nelissen BJM, Reekmans RJ;
 XX WPI; 2001-367042/38.
 DR N-PSpb; AAI29869.

XX PT Yeast and fungal nucleic acids encoding proteins involved in a pathway
 PT leading to programmed cell death, useful for treating proliferative
 PT disorders, yeast and fungal infections, or for preventing apoptosis in
 PT certain diseases.
 XX PS Claim 24; Fig 2; 218pp; English.
 XX The present invention provides the protein and coding sequences of a
 CC number of apoptosis associated proteins from the yeast *Saccharomyces*
 CC cerevisiae and the fungus *Candida albicans*. These can be used to identify
 CC treatments for fungal and yeast infections, for proliferative diseases
 CC and for apoptosis related diseases such as autoimmune diseases, ischaemia
 CC and neurodegeneration. The present sequence is one of the *C. albicans*
 CC proteins of the invention.

XX Sequence 796 AA;
 XX Query Match 91.2%; Score 31; DB 4; Length 796;
 Best Local Similarity 83.3%; Pred. No. 1.6e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DGDGFA 6
 |||||:
 Db 78 DGDGFA 83

Search completed: June 1, 2004, 18:08:38
 Job time : 57 secs

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OM protein - protein search, using SW model

Run on: June 1, 2004, 18:07:34 ; Search time 23 Seconds

(without alignments)

13.468 Million cell updates/sec

Title: US-09-715-763A-5

Perfect score: 34

Sequence: 1 DGDGFA 6

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgnd_6/ptodata/2/iaa/5A_COMB_pep:*

2: /cgnd_6/ptodata/2/iaa/5B_COMB_pep:*

3: /cgnd_6/ptodata/2/iaa/6A_COMB_pep:*

4: /cgnd_6/ptodata/2/iaa/6B_COMB_pep:*

5: /cgnd_6/ptodata/2/iaa/PCUTS_COMB_pep:*

6: /cgnd_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91.2	268	4	US-09-252-991A-21630	Sequence 21630, A
2	91.2	288	4	US-09-134-001C-4969	Sequence 4969, A
3	88.2	81	4	US-09-137-522A-3839	Sequence 3839, A
4	88.2	116	4	US-09-489-039A-7242	Sequence 7242, A
5	88.2	122	4	US-09-107-532A-5730	Sequence 5730, A
6	88.2	219	4	US-09-205-258-271	Sequence 271, A
7	88.2	264	4	US-09-252-991A-19619	Sequence 19619, A
8	88.2	291	4	US-09-252-991A-25517	Sequence 25517, A
9	88.2	331	2	US-08-910-927B-5	Sequence 3, A
10	88.2	331	3	US-09-206-499-3	Sequence 5, A
11	88.2	331	3	US-09-270-270-5	Sequence 3, A
12	88.2	356	4	US-09-540-236-3392	Sequence 3392, A
13	88.2	367	4	US-09-404-296B-6	Sequence 6, A
14	88.2	381	4	US-09-328-352-4500	Sequence 4500, A
15	88.2	478	4	US-09-489-039A-12483	Sequence 12483, A
16	88.2	496	4	US-09-312-76A-15	Sequence 15, A
17	88.2	520	4	US-09-252-991A-17342	Sequence 17342, A
18	88.2	529	1	US-08-178-47B-32	Sequence 32, A
19	88.2	529	4	US-09-304-12A-2	Sequence 2, A
20	88.2	573	4	US-09-252-991A-31334	Sequence 31334, A
21	88.2	748	4	US-09-134-000C-6041	Sequence 6041, A
22	88.2	782	4	US-09-360-548-16	Sequence 16, A
23	88.2	782	4	US-09-398-39A-46	Sequence 46, A
24	88.2	782	4	US-09-887-58A-46	Sequence 46, A
25	88.2	782	4	US-09-895-75A-46	Sequence 46, A
26	88.2	782	4	US-09-903-01B-46	Sequence 46, A
27	88.2	782	4	US-09-903-01B-46	Sequence 46, A

Title:	US-09-715-763A-5	Score:	28	30	88.2	782	4	US-09-900-797-46
Perfect score:	34	29	30	88.2	783	4	US-09-513-783A-176	
Sequence:	1 DGDGFA 6	31	30	88.2	817	3	US-09-234-393-13	
Scoring table:	BLOSUM62	32	30	88.2	817	3	US-09-234-393-40	
Gapext:	0.5	33	30	88.2	817	3	US-09-234-393-42	
Searched:	389414 seqs, 51625971 residues	34	30	88.2	817	4	US-09-865-171-43	
Total number of hits satisfying chosen parameters:	389414	35	30	88.2	817	4	US-09-865-171-38	
Minimum DB seq length:	0	36	30	88.2	817	4	US-09-865-171-40	
Maximum DB seq length:	2000000000	37	30	88.2	817	4	US-09-865-171-42	

ALIGNMENTS

RESULT 1									
US-09-252-991A-21630									
; Sequence 21630, Application US/09252991A									
; Parent No: 6551795									
; GENERAL INFORMATION:									
; APPLICANT: Marc J. Rubenfeld et al.									
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS									
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS									
; FILE REFERENCE: 107196-136									
; CURRENT APPLICATION NUMBER: US/09-252-991A									
; CURRENT FILING DATE: 1999-02-18									
; PRIOR APPLICATION NUMBER: US 60/074,788									
; PRIOR FILING DATE: 1998-02-18									
; PRIOR APPLICATION NUMBER: US 60/094,190									
; PRIOR FILING DATE: 1998-07-27									
; NUMBER OF SEQ ID NOS: 33142									
; SEQ ID NO: 21630									
; LENGTH: 268									
; TYPE: PRT									
; ORGANISM: Pseudomonas aeruginosa									
US-09-252-991A-21630									
Query Match	91.2%	Score	31;	DB 4;	Length	268;			
Best Local Similarity	83.3%	Pred.	No.	1.6e+02;	Mismatches	1;	Indels	0;	Gaps
Matches	5;	Conservative							
OY	1	DGDGRA	6						
Db	;								
	37	DGDGFS	42						

RESULT 2									
US-09-134-001C-4969									
; Sequence 4969, Application US/09134001C									
; Patent No: 6380370									
; GENERAL INFORMATION:									
; APPLICANT: Lynn Doucette-Stamm et al									
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS									
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS									
; FILE REFERENCE: GNC-007									
; CURRENT APPLICATION NUMBER: US/09/134-001C									
; CURRENT FILING DATE: 1998-08-13									
; PRIOR APPLICATION NUMBER: US 60/064,964									
; PRIOR FILING DATE: 1997-11-08									
; PRIOR APPLICATION NUMBER: US 60/055,779									
; PRIOR FILING DATE: 1997-08-14									
; NUMBER OF SEQ ID NOS: 5674									
; SEQ ID NO: 4969									
; LENGTH: 288									
; TYPE: PRT									

Result No.	Score	Query Match	Length	DB ID	Description
1	91.2	268	4	US-09-252-991A-21630	Sequence 21630, A
2	91.2	288	4	US-09-134-001C-4969	Sequence 4969, A
3	88.2	81	4	US-09-137-522A-3839	Sequence 3839, A
4	88.2	116	4	US-09-489-039A-7242	Sequence 7242, A
5	88.2	122	4	US-09-107-532A-5730	Sequence 5730, A
6	88.2	219	4	US-09-205-258-271	Sequence 271, A
7	88.2	264	4	US-09-252-991A-19619	Sequence 19619, A
8	88.2	291	4	US-09-252-991A-25517	Sequence 25517, A
9	88.2	331	2	US-08-910-927B-5	Sequence 3, A
10	88.2	331	3	US-09-206-499-3	Sequence 5, A
11	88.2	331	3	US-09-270-270-5	Sequence 3, A
12	88.2	356	4	US-09-540-236-3392	Sequence 3392, A
13	88.2	367	4	US-09-404-296B-6	Sequence 6, A
14	88.2	381	4	US-09-328-352-4500	Sequence 4500, A
15	88.2	478	4	US-09-489-039A-12483	Sequence 12483, A
16	88.2	496	4	US-09-312-76A-15	Sequence 15, A
17	88.2	520	4	US-09-252-991A-17342	Sequence 17342, A
18	88.2	529	1	US-08-178-47B-32	Sequence 32, A
19	88.2	529	4	US-09-304-12A-2	Sequence 2, A
20	88.2	573	4	US-09-252-991A-31334	Sequence 31334, A
21	88.2	748	4	US-09-134-000C-6041	Sequence 6041, A
22	88.2	782	4	US-09-360-548-16	Sequence 16, A
23	88.2	782	4	US-09-398-39A-46	Sequence 46, A
24	88.2	782	4	US-09-887-58A-46	Sequence 46, A
25	88.2	782	4	US-09-895-75A-46	Sequence 46, A
26	88.2	782	4	US-09-903-01B-46	Sequence 46, A
27	88.2	782	4	US-09-903-01B-46	Sequence 46, A

ORGANISM: *Staphylococcus epidermidis*
US-09-134-001C-4969

Query Match 91.2%; Score 31; DB 4; Length 288;
Best Local Similarity 83.3%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 DGDGFA 6
Db 92 DGDGYA 97

RESULT 3
US-09-107-532A-3839
Sequence 3839; Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts

COUNTRY: USA
ZIP: 02454

COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598

FILING DATE: 30-Jun-1998

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 3839:

SEQUENCE CHARACTERISTICS:

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1.. 81

SEQUENCE DESCRIPTION: SEQ ID NO: 3839:

Query Match 88.2%; Score 30; DB 4; Length 81;

Best Local Similarity 100.0%; Pred. No. 67; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGDGF 5
Db 50 DGDGF 54

US-09-489-039A-7242
Sequence 039A-7242; Application US/09489039A
Patent No. 6610866
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709_2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO: 7242
LENGTH: 116
TYPE: PRT
ORGANISM: *Klebsiella pneumoniae*
US-09-489-039A-7242
Query Match 88.2%; Score 30; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 98; Mismatches 0; Indels 0; Gaps 0;
QY 1 DGDF 5
Db 51 DGDF 55

RESULT 5
US-09-107-532A-5730
Sequence 5730; Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02454
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
PRIORITY NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3839:
SEQUENCE CHARACTERISTICS:
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium

FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1.. 81
SEQUENCE DESCRIPTION: SEQ ID NO: 3839:

Query Match 88.2%; Score 30; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 67; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGDF 5
Db 50 DGDF 54

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (B) LOCATION 1..122
 SEQUENCE DESCRIPTION: SEQ ID NO: 5730:

Query Match 88.2%; Score 30; DB 4; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DGDGPF 5
 Db 66 DGDGPF 70

RESULT 6
 US-09-205-258-271
 ; Sequence 271, Application US/09205258
 ; Patent No. 6525174
 ; GENERAL INFORMATION:
 ; APPLICANT: Young et al.
 ; TITLE OF INVENTION: 207 Human Secreted Proteins
 ; FILE REFERENCE: PZ007P1
 ; CURRENT APPLICATION NUMBER: US/09/205, 258
 ; CURRENT FILING DATE: 1998-12-04
 ; EARLIER APPLICATION NUMBER: PCT/US98/11422
 ; EARLIER FILING DATE: 1998-06-04
 ; EARLIER APPLICATION NUMBER: 60/048, 885
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/049, 375
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 881
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 880
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 896
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/049, 020
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 876
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 895
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 884
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 882
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 899
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 893
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 900
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 901
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 892
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 915
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/049, 019
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 970
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 972
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 916
 ; EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049, 373
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 875
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/049, 374
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 949
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 974
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 883
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 897
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 898
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 962
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 963
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 877
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 878
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048, 923
 ; EARLIER FILING DATE: 1997-12-18
 ; EARLIER APPLICATION NUMBER: 60/092, 921
 ; EARLIER FILING DATE: 1998-07-15
 ; EARLIER APPLICATION NUMBER: 60/094, 657
 ; EARLIER FILING DATE: 1998-07-30
 ; NUMBER OF SEQ ID NOS: 1227
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 271
 ; LENGTH: 219
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (219)
 ; OTHER INFORMATION: Xaa equals stop translation

US-09-205-258-271

Query Match 88.2%; Score 30; DB 4; Length 219;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DGDGPF 5
 Db 200 DGDGPF 204

RESULT 7
 US-09-252-991A-19619
 ; Sequence 19619, Application US/09252991A
 ; Patent No. 6551195
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenstein et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 101196_136
 ; CURRENT APPLICATION NUMBER: US/09/252, 991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074, 748
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094, 190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 19619
 ; LENGTH: 264
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-19619
 Query Match Similarity 88.2%; Score 30; DB 4; Length 264;
 * Best Local Similarity 100.0%; Pred. No. 2.3e+02; Length 264;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DGDGF 5
 Db 98 |||||
 DGDGF 102

RESULT 8
 US-09-252-991A-25517
 ; Sequence 25517, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenstein et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AFRGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 25517
 ; LENGTH: 91
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-25517

Query Match Similarity 88.2%; Score 30; DB 4; Length 291;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02; Length 291;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DGDGF 5
 Db 168 |||||
 DGDGF 172

RESULT 9
 US-09-828-242-3
 ; Sequence 3, Application US/08828242
 ; Patent No. 5871970
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Goli, Surya K.
 ; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
 ; TITLE OF INVENTION: PROTEIN
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/910,927B
 FILING DATE: Herewith
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0358 US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 331 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1262329

US-08-910-927B-5
 Query Match Score 30; DB 2; Length 331;
 Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Number of Sequences: 6

QY 1 DGDF 5
 Db 94 DGDGF 98

RESULT 11
 US-09-206-499-3
 Sequence 3, Application US/09206499
 i General Information:
 i Patent No. 6194385
 i APPLICANT: Hillman, Jennifer L.
 i APPLICANT: Goli, Surya K.
 i TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEIN
 i NUMBER OF SEQUENCES: 4
 i CORRESPONDENCE ADDRESS:
 i ADDRESSEE: Incyte Pharmaceuticals, Inc.
 i STREET: 3174 Porter Drive
 i CITY: Palo Alto
 i STATE: CA
 i COUNTRY: USA
 i ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/270,270
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/910,927
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0358 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 331 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1262329
 US-09-270-270-5

Query Match Score 88.2%; Score 30; DB 3; Length 331;
 Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Number of Sequences: 6

QY 1 DGDF 5
 Db 94 DGDGF 98

RESULT 12
 US-09-270-270-5
 Sequence 5, Application US/09270270
 i General Information:
 i Patent No. 623547
 i TITLE OF INVENTION: MORAXELLA CATARRHALIS
 i NUMBER OF SEQUENCES: 6

Query Match Score 88.2%; Score 30; DB 4; Length 356;
 Best Local Similarity 100.0%; Pred. No. 3.e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DGDGF 5
 Db 225 DGDGF 229

RESULT 14
 US-09-404-296B-6
 ; Sequence 6, Application US/09404296B
 ; GENERAL INFORMATION:
 ; APPLICANT: MURRAY, James Augustus Henry
 ; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
 ; FILE REFERENCE: 2121-0151P
 ; CURRENT APPLICATION NUMBER: US/09/404,296B
 ; CURRENT FILING DATE: 1999-03-24
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 367
 ; TYPE: PRT
 ; ORGANISM: Nicotiana tabacum
 US-09-404-296B-6

Query Match 88.2%; Score 30; DB 4; Length 367;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DGDGF 5
 Db 82 DGDGF 86

RESULT 15
 US-09-328-352-4500
 ; Sequence 4500, Application US/09328352
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTCS9-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 4500
 ; LENGTH: 381
 ; TYPE: PRT
 ; ORGANISM: Acinetobacter baumannii
 US-09-328-352-4500

Query Match 88.2%; Score 30; DB 4; Length 381;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DGDGF 5
 Db 40 DGDGF 44

Search completed: June 1, 2004, 18:11:02
 Job time : 24 secs

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OM Protein - protein search, using sw model

Run on: June 1, 2004, 18:08:44 ; Search time 43 Seconds

(without alignments)
38.965 Million cell updates/sec

Title: US-09-715-763A-5

Perfect score: 34

Sequence: 1 DGDGA, 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1151071 seqs, 27924946 residues

Total number of hits satisfying chosen parameters:

1151071

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : Published Applications AA:*

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15: /cnm2_6/_ptodata/1/_pubpa/US10C_PUBCCOMB.pep:*

16: /cnm2_6/_ptodata/1/_pubpa/US10C_PUBCCOMB.pep:*

17: /cgnd_6/_ptodata/1/_pubpa/US10I_NEW_PUB.pep:*

18: /cgnd_6/_ptodata/1/_pubpa/US09_PUBCCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	34	100.0	237	12 US-10-335-977-6441 Sequence 6441, AP
2	34	100.0	238	12 US-10-335-977-6440 Sequence 6440, AP
3	34	100.0	260	12 US-10-335-977-6442 Sequence 6442, AP
4	34	100.0	273	12 US-10-335-977-6443 Sequence 6443, AP
5	34	100.0	326	12 US-10-282-122A-42291 Sequence 42291, A
6	34	100.0	523	12 US-10-424-599-240458 Sequence 240458, AP
7	31	91.2	475	14 US-10-156-761-12821 Sequence 12821, A
8	31	91.2	481	14 US-10-156-761-12010 Sequence 12010, A
9	31	91.2	489	14 US-10-156-761-8688 Sequence 8688, AP
10	31	91.2	763	12 US-10-282-122A-4839 Sequence 4839, A
11	30	88.2	53	9 US-09-864-498A-416 Sequence 38025, A
12	30	88.2	63	11 US-09-864-498A-416 Sequence 416, APP
13	30	88.2	65	12 US-10-124-599-271030 Sequence 271030, APP
14	30	88.2	70	14 US-10-156-761-103117 Sequence 103117, A
15	30	88.2	76	12 US-10-424-599-255937 Sequence 255937, A

CURRENT APPLICATION DATA:

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: Windows NT 4.0

SOFTWARE: UNIX

CURRENT ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: US/10/315, 977

FILING DATE: 30-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/993, 002

FILING DATE: 17-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36, 207

REFERENCE/DOCKET NUMBER: GTIN-018

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 6441:

SEQUENCE CHARACTERISTICS:

LENGTH: 237 amino acids

RESULT 1

US-10-335-977-6441

; Sequence 6441, Application US/10335977

; Publication No. US2004052799A1

; GENERAL INFORMATION:

; APPLICANT: DOUGLAS SMITH et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 10031

; CORRESPONDENCE ADDRESS: LAHIVE & COCKFIELD

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori

FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...237;
SEQUENCE DESCRIPTION: SEQ ID NO: 6441;
US-10-335-977-6441

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Indels	Gaps
Qy	100.0%	DB 12;	237;	100.0%	1e+02;	0;	0;	0;
Db	81	DGDGFA 6		6;	Conservative	0;	Mismatches	0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...237;
SEQUENCE DESCRIPTION: SEQ ID NO: 6441;
US-10-335-977-6441

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Indels	Gaps
Qy	100.0%	DB 12;	237;	100.0%	1e+02;	0;	0;	0;
Db	81	DGDGFA 86		6;	Conservative	0;	Mismatches	0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-10-335-977-6442
Sequence 6442, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,2,07
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 6442:
SEQUENCE CHARACTERISTICS:
LENGTH: 260 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...260
SEQUENCE DESCRIPTION: SEQ ID NO: 6442;
US-10-335-977-6442

Query Match 100.0%; Score 34; DB 12; Length 260;
Best Local Similarity 10.0%; Pred. No. 1.e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DGDGFA 6
Db 82 DGDGFA 87

FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...228
SEQUENCE DESCRIPTION: SEQ ID NO: 6440;
US-10-335-977-6440

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Indels	Gaps
Qy	100.0%	DB 12;	238;	100.0%	1e+02;	0;	Mismatches	0;
Db	82	DGDGFA 87		6;	Conservative	0;	Indels	0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-10-335-977-6443
Sequence 6443, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:

ADDRESSEES: LAHIVE & COCKFIELD

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: Windows NT 4.0

SOFTWARE: UNIX

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/335,977

FILING DATE: 30-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/993,002

FILING DATE: 17-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: GTN-018

TELECOMMUNICATION INFORMATION:

TELEFAX: (617)227-4400

INFORMATION FOR SEQ ID NO: 6443:

SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE: Helicobacter pylori

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...273

SEQUENCE DESCRIPTION: SEQ ID NO: 6443:

Query Match

Score 34;

DB 12;

Length 273;

Best Local Similarity 100.0%;

Pred. No. 1.2e+02;

Mismatches 0;

Indels 0;

Gaps 0;

Qy 1 DGDGFA 6

Db 95 DGDGFA 100

RESULT 5
US-10-335-977-6443
Query Match

Score 34;

DB 12;

Length 273;

Best Local Similarity 100.0%;

Pred. No. 1.2e+02;

Mismatches 0;

Indels 0;

Gaps 0;

Qy 1 DGDGFA 6

Db 95 DGDGFA 100

RESULT 5
US-10-282-122A-42991
Query Match

Score 34;

DB 12;

Length 523;

Best Local Similarity 100.0%;

Pred. No. 2.3e+02;

Mismatches 0;

Indels 0;

Gaps 0;

Qy 1 DGDGFA 6

Db 365 DGDGFA 370

PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SEQ ID NO: 42991
TYPE: PRT
ORGANISM: Escherichia coli
US-10-282-122A-42991
Query Match

Best Local Similarity 100.0%;
Matches 6; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;
Qy 1 DGDGFA 6
Db 78 DGDGFA 83

RESULT 6
US-10-424-599-240458
Sequence 240458, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J

APPLICANT: Kovalic, David K

APPLICANT: Zhou Yinua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(5323)B

CURRENT APPLICATION NUMBER: US/10/424-599

CURRENT FILING DATE: 2003-04-28

SEQ ID NO: 285684

LENGTH: 523

TYPE: PRT

ORGANISM: Glycine max

FEATURE: NAME/KEY: unsure

LOCATION: (1)...(523)

OTHER INFORMATION: unsure at all Xaa locations

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_59160C.1.pep

US-10-424-599-240458

Query Match

Best Local Similarity 100.0%;
Matches 6; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 1 DGDGFA 6

Db 365 DGDGFA 370

RESULT 5
US-10-282-122A-42991
Query Match

Score 34;

DB 12;

Length 523;

Best Local Similarity 100.0%;

Pred. No. 2.3e+02;

Mismatches 0;

Indels 0;

Gaps 0;

Qy 1 DGDGFA 6

Db 365 DGDGFA 370

RESULT 7 US-10-156-761-12821
 Sequence 12821, Application US/10156761
 Publication No. US20030119018A1
 GENERAL INFORMATION:
 APPLICANT: OMURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIOUKI
 APPLICANT: HATTORI, MASAHIRO
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 SEQ ID NO 12821
 PRIORITY NUMBER: JP 2001-272697
 PRIORITY FILING DATE: 2001-08-02
 SEQ ID NO 12821
 LENGTH: 475
 TYPE: PRT
 ORGANISM: Streptomyces avermitilis
 US-10-156-761-12821

Query Match 91.2%; Score 31; DB 14; Length 475;
 Best Local Similarity 83.3%; Pred. No. 7.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 DGDEFA 6
 Db 121 DGDFGS 126

RESULT 8 US-10-156-761-12010
 Sequence 12010, Application US/10156761
 Publication No. US20030119018A1
 GENERAL INFORMATION:
 APPLICANT: OMURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIOUKI
 APPLICANT: HATTORI, MASAHIRO
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 SEQ ID NO 12010
 LENGTH: 481
 TYPE: PRT
 ORGANISM: Streptomyces avermitilis
 US-10-156-761-12010

Query Match 91.2%; Score 31; DB 14; Length 481;
 Best Local Similarity 83.3%; Pred. No. 7.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 DGDEFA 6
 Db 106 DGDFYA 111

RESULT 9 US-10-156-761-8688
 Sequence 8688, Application US/10156761
 Publication No. US20030119018A1
 GENERAL INFORMATION:
 APPLICANT: OMURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIOUKI
 APPLICANT: HATTORI, MASAHIRO
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 SEQ ID NO 8688
 LENGTH: 489
 TYPE: PRT
 ORGANISM: Streptomyces avermitilis
 US-10-156-761-8688

Query Match 91.2%; Score 31; DB 14; Length 489;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 DGDGFA 6
 Db 360 DGDFYA 365

RESULT 10 US-10-281-122A-48639
 Sequence 48639, Application US/10282122A
 Publication No. US20040029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-11
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 48639
; LENGTH: 763
; TYPE: PRT
; ORGANISM: *Bacteroides fragilis*
; US-10-282-122A-48639

Query Match 91.2%; Score 31; DB 12; Length 763;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DGDGFA 6
Db 292 DGDGFS 297

RESULT 11
US-09-864-761-38025
; Sequence 38025, Application US/09864761
; Patent No. US2004008763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharren G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE EXPRESSION: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/224,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/508,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 38025
; LENGTH: 53
; TYPE: PRT
; ORGANISM: *Homo sapiens*
; FEATURE:
; OTHER INFORMATION: MAP TO AC009948.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
; OTHER INFORMATION: SWISSPROT HIT: Q62703, EVALUE 6.805e-01
; OTHER INFORMATION: EST_HUMAN HIT: AI271550.1, EVALUE 8.00e-26
; US-09-864-761-38025
Query Match 88.2%; Score 30; DB 9; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DGDGFS 5
Db 35 DGDGFS 39

RESULT 12
US-09-864-408A-416
; Sequence 416, Application US/09864408A
; Publication No. US2004009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shirkets, Richard A.
; TITLE OF INVENTION: No. US2004009474A1 Human Polynucleotides and Polypeptides Encoded by Human Polynucleotides
; FILE REFERENCE: 214002-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 416
; LENGTH: 63
; TYPE: PRT
; ORGANISM: *Homo sapiens*
; US-09-864-408A-416
Query Match 88.2%; Score 30; DB 11; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DGDGFS 5
Db 11 DGDGFS 15

RESULT 13
US-10-424-599-271030
; Sequence 271030, Application US/10424599
; Publication No. US2004001072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (5323) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO: 271030
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Glycine max

RESULT 14
US-10-156-761-10317
; Sequence 10317, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADASHI
; APPLICANT: SAKAKI, YOSHIOUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; CURRENT APPLICATION NUMBER: US/10/156,761
; FILE REFERENCE: 249-262
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO: 10317
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10317

Query Match 88.2%; Score 30; DB 14; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Missmatches 0; Indels 0; Gaps 0;

Qy 1 DGDFG 5
Db 55 DGDF 59

Search completed: June 1, 2004, 18:11:58
Job time : 44 secs

RESULT 15
US-10-424-599-255937
; Sequence 255937, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO: 255937
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:

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OM protein - protein search, using sw model

Run on: June 1, 2004, 18:06:04 ; Search time 21 Seconds

(without alignments)
27.483 Million cell updates/sec

Title: US-09-715-763A-5

Perfect score: 34
Sequence: 1 DGDGFA 6Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: pir1;*

2: pir2;*

3: pir3;*

4: pir4;*

RESULT 1
P64593

Pyruvate Synthase (EC 1.2.7.1) beta chain - Helicobacter pylori (strain 26695)

C.Species: Helicobacter pylori

C.Date: 10-Sep-1999 #sequence_change 05-May-2000

C.Accession: F64593

P;Tomb, J. P.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McGenney, J.D.; Kelley, J.M.; Cottrell, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.A.

B;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; PMID:97394467; PMID:3252185

A;Accession: P64593

A;Status: Preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Cross-references: GB:AE000572; GB:AE000511; NID:92313703; PIDN:AAD07655.1; PID:92313705

C;Keywords: coenzyme A; oxidoreductase

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB	ID	Description
1	34	100.0	273	1	F64593	pyruvate synthase
2	34	100.0	273	2	H1919	chain of 2-oxoglutarate synthase
3	34	100.0	288	2	E83946	pyruvate synthase
4	34	100.0	310	2	C95950	conserved hypothetical protein
5	34	100.0	310	2	T35417	probable beta-lactamase
6	34	100.0	314	2	AC2879	aromatic compounds ABC transporter homolog
7	34	100.0	325	2	B97654	hypothetical protein
8	34	100.0	326	2	B91100	hypothetical protein
9	34	100.0	326	2	F85945	hypothetical protein
10	34	100.0	326	2	B65074	hypothetical protein
11	34	100.0	536	2	D84325	Htr17 transducer
12	34	100.0	627	2	F84194	Htr14 transducer
13	34	100.0	764	2	A84328	Htr2 transducer
14	34	100.0	765	1	T44916	transducer protein
15	34	100.0	777	2	T44597	transducer protein
16	34	100.0	778	2	T48887	transducer protein
17	34	100.0	778	2	F84237	Htr4 transducer
18	34	100.0	788	2	T44622	transducer protein
19	34	100.0	789	2	E84226	Htr6 transducer
20	31	91.2	262	2	T17935	ankyrin repeat protein
21	31	91.2	267	2	C83242	conserved hypothetical protein
22	31	91.2	288	2	E89903	hypothetical protein
23	31	91.2	339	2	T28128	Ig V-region-like B
24	31	91.2	340	2	T28137	Ig V-region-like B
25	31	91.2	372	2	C39311	Ig V-region-like B
26	31	91.2	536	1	A41790	Htr1 transducer
27	31	91.2	536	2	E83318	hypothetical protein
28	31	91.2	1025	2	AE2243	cell surface glycoprotein
29	31	91.2	1408	2	H69068	Superfamily: pyruvate synthase beta chain

ALIGNMENTS

Query Match	Best Local Similarity	Score	DB 1	Length
Matches 6;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy 1 DGDGFA 6				
Db 95 DGDGFA 100				
RESULT 2				
Chain of 2-oxoglutarate oxidoreductase - Helicobacter pylori (strain J99)				
C.Species: Helicobacter pylori				
A;Variety: strain J99				
C;Accession: H71919				
C;Cross-references: GB:AE001486; ARN>				
A;Molecule type: DNA				
A;Accession: H71919				
A;Status: Preliminary				
A;Keywords: coenzyme A; oxidoreductase				
RESULT 3				
Chain of 2-oxoglutarate oxidoreductase - Helicobacter pylori (strain J99)				
C.Species: Helicobacter pylori				
A;Variety: strain J99				
C;Accession: H71919				
C;Cross-references: GB:AE001486; ARN>				
A;Molecule type: DNA				
A;Accession: H71919				
A;Status: Preliminary				
A;Keywords: coenzyme A; oxidoreductase				

Query Match 100.0%; Score 34; DB 2; Length 273;
 Best Local Similarity 100.0%; Pred. No. 22; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 123 DGDGFA 128

RESULT 5
 T35417 probable beta-lactamase - *Streptomyces coelicolor*
 C;Species: *Streptomyces coelicolor*
 C;Date: 05-Nov-1999 #text_change 05-Nov-1999
 C;Accession: T35417
 R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, March 1999
 A;Reference number: Z21577
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-310 <OLI>
 A;Cross-references: EMBL:AL049485; PIDN:CAB39710.1; GSPDB:GN00070; SCOECDB:SC6A5 26C
 A;Experimental source: strain A3 (2)
 C;Genetics:
 A;Gene: SCOECDB:SC6A5..26C

Query Match 100.0%; Score 34; DB 2; Length 310;
 Best Local Similarity 100.0%; Pred. No. 25; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DGDGFA 6
 Db 295 DGDGFA 300

Query Match 100.0%; Score 34; DB 2; Length 310;
 Best Local Similarity 100.0%; Pred. No. 25; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DGDGFA 6
 Db 295 DGDGFA 300

RESULT 6
 AC2878 aromatic compounds dioxygenase [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont
 aromatic compounds dioxygenase [imported] - *Agrobacterium tumefaciens*
 C;Species: *Agrobacterium tumefaciens*
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C;Accession: AC2878
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
 erge, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Author: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Perry, M.; Gordon-Kamm, F.
 ster, E.W.
 A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: AC2878
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-314 <KUR>
 A;Cross-references: GB:AE0008688; PIDN:AAL43441.1; PID:917740944; GSPPDB:GN00186
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:

A;Gene: ACU2453
 A;Map position: circular chromosome
 C;Superfamily: *Bacillus subtilis* probable ABC transporter ydfo

Query Match 100.0%; Score 34; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. No. 25; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DGDGFA 6
 Db 123 DGDGFA 128

RESULT 7
 B97654 ABC transporter homolog ydfo [imported] - *Agrobacterium tumefaciens* (strain C58, Cereon)
 C;Species: *Agrobacterium tumefaciens*
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
 C;Accession: E97654
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Scott, C.; Lappas, C.; Markez, B.;
 Science 294, 2323-2328, 2001

Query Match 100.0%; Score 34; DB 2; Length 310;
 Best Local Similarity 100.0%; Pred. No. 25; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DGDGFA 6
 Db 123 DGDGFA 128

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebbhardt, H.; Lowe, T.M.; Li
 A; Title: Genome sequence of Halobacterium species NRC-1.
 A; Reference number: A84160; MUID:20504483; PMID:11016950
 A; Accession: F84194
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-627 <STO>
 A; Cross-references: GB:AE004437; PIDN:AGI18922.1; GSPDB:GN00138
 C; Genetics:
 A; Gene: htrII
 C; Superfamily: Halobacterium salinarum transducer protein htrII

Query Match 100.0%; Score 34; DB 2; Length 627;
 Best Local Similarity 100.0%; Pred. No. 51; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Gaps 0;

RESULT 15
 T44597

transducer protein httpV [similarity] - Halobacterium salinarum

A; Description: involved in phototactic signal transduction from sensory rhodopsin II (PRI
 C; Function: involved in phototactic signal transduction from sensory rhodopsin II (PRI
 A; Note: the adaptation response is mediated by methylation of the transducer protein htrII
 C; Superfamily: Halobacterium salinarum transducer protein htrII
 C; Keywords: methyl-accepting transducer protein htrII
 F;481-733/Region: MCP signalling domain similarity

Query Match 100.0%; Score 34; DB 1; Length 765;

Best Local Similarity 100.0%; Pred. No. 63; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 DGDGFA 6
 Db 603 DGDGFA 608

RESULT 16
 T44597

transducer protein httpV [similarity] - Halobacterium salinarum

A; Description: methyl-accepting transducer protein htrII; transducer protein httpV

C; Species: Halobacterium salinarum

C; Accession: F44597

R;Zhang, W.; Brooun, A.; McCandless, J.; Banda, P.; Alam, M.

Proc. Natl. Acad. Sci. U.S.A. 93, 4649-4654, 1996

C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Sep-2000

C; Cross-references: EMBL:U75438; NID:91654424; PIDN:AAB17883.1; PMID:8643458

A; Title: Signal transduction in the archaeon Halobacterium salinarum is processed through

A; Reference number: 222804; MUID:96209786; PMID:96209786

A; Status: preliminary; translated from GB/EMBL/DBJ

A; Molecule type: DNA

A; Residues: 1-777 <ZHA>

A; Cross-references: EMBL:U75438; NID:91654424; PIDN:AAB17883.1; PMID:9643458

A; Experimental source: strain mFx15

A; Note: the source is designated as Halobacterium salinarum

C; Genetics:

A; Gene: httpV; http6; htrII

C; Keywords: methyl-ated amino acid; signal transduction; transmembrane protein

F;494-746/Region: MCP signalling domain similarity

Query Match 100.0%; Score 34; DB 2; Length 777;

Best Local Similarity 100.0%; Pred. No. 64; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 DGDGFA 6
 Db 616 DGDGFA 621

Search completed: June 1, 2004, 18:10:27

Job time : 23 secs

RESULT 14

T44946

transducer protein htrII [validated] - Halobacterium salinarum

N; Alternative names: methyl-accepting taxis protein htrII; transducer protein http2

C; Species: Halobacterium salinarum

C; Accession: T44946

R;Zhang, W.; Brooun, A.; Mueller, M.M.; Alam, M.

Proc. Natl. Acad. Sci. U.S.A. 93, 8230-8235, 1996

A; Title: The primary structures in the Archaeon Halobacterium salinarum blue light rece

A; Reference number: Z22877; MUID:9623203; PMID:8710852

A; Status: preliminary; translated from GB/EMBL/DBJ

A; Molecule type: DNA

A; Residues: 1-765 <ZHA>

A; Cross-references: EMBL:U62676; PIDN: AAC44369.1

A; Experimental source: strain mFx15

A; Note: the source is designated as Halobacterium salinarum

C; Genetics:

A; Gene: htrII; http2

Result No.	Score	Query Match Length	DB ID	Description
SUMMARIES				
1	34	100.0	325	1 UP14_ECOLI
2	34	100.0	763	1 HTR2_HALSA
3	34	100.0	764	1 HTR2_HALSA
4	34	100.0	778	1 HTR6_HALSA
5	34	100.0	778	1 HTR6_HALSA
6	31	91.2	535	1 HTR1_HALSA
7	31	91.2	535	1 HTR1_HALSA
8	30	88.2	78	1 POC7_PHLPR
9	30	88.2	80	1 POC7_CYND
10	30	88.2	81	1 POC3_SYRVO
11	30	88.2	88	1 POC3_OLEEU
12	30	88.2	85	1 POC4_ALNGU
13	30	88.2	85	1 POC4_BETVE
14	30	88.2	148	1 CALL_DROME
15	30	88.2	148	1 CALM_METSER
16	30	88.2	148	1 CALM_PATESP
17	30	88.2	214	1 HS30_ONCITS
18	30	88.2	259	1 FKB7_HUMAN
19	30	88.2	311	1 RCN1_HUMAN
20	30	88.2	340	1 YMDF7_YEAST
21	30	88.2	389	1 TAL_GLOVI
22	30	88.2	391	1 TAL_SYN3
23	30	88.2	402	1 PGH1_ERMCIA
24	30	88.2	402	1 PGH2_ERMCIA
25	30	88.2	433	1 HTR2_HALVA
26	30	88.2	438	1 POHO_PSPAE
27	30	88.2	444	1 GID_STRR6
28	30	88.2	468	1 AMFB_BACFI
29	30	88.2	472	1 RE16_SCHPO
30	30	88.2	477	1 FES_FSVST
31	30	88.2	494	1 TCN1_STRGA
32	30	88.2	529	1 HSF1_HUMAN
33	30	88.2	559	1 PMGI_MAIZE

Scoring table: BL2USM62
Gapop 10.0 , Gapext 0.5
Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries
Database : Swissprot_42:*

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description	SEQUENCE FROM N.A.
1	34	100.0	325	1 UP14_ECOLI	SPECIES=E.coli; STRAIN=K12 / MG1655; RC MEDLINE=9426617; PubMed=9278503;
2	34	100.0	763	1 HTR2_HALSA	RA Blattner R.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V., RA Riley M., Collado-Vides J., Glasner J.D., Rose C.K., Mayhew G.F., RA Gregor J.J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., RA Mau B., Shao Y.; RT "The complete genome sequence of Escherichia coli K-12."; RN [1]
3	34	100.0	764	1 HTR2_HALSA	RC SEQUENCE OF 1-12. RX MEDLINE=7443975; PubMed=9288646; RN [2]
4	34	100.0	778	1 HTR6_HALSA	RA Link A.J., Robison K., Church G.M.; RT "Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12."; RL Electrophoresis 18:1259-1313 (1997). RN [3]
5	34	100.0	778	1 HTR6_HALSA	RC SEQUENCE FROM N.A. SPECIES=S.flexneri; STRAIN=301 / Serotype 2a; RC MEDLINE=22406; PubMed=12384530;
6	31	91.2	535	1 HTR1_HALSA	RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y., RA Yu J.; RT "Genome sequence of shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157:H7"; RL Nucleic Acids Res. 30:4432-4441 (2002). RN [4]
7	31	91.2	535	1 HTR1_HALSA	RC SEQUENCE FROM N.A. SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a; RC MEDLINE=2259074; PubMed=12704152;
8	30	88.2	78	1 POC7_PHLPR	RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., RA Fournier G., Mayhew G.P., Plunkett G., III, Rose D.J., Darling A., RA Mau B., Perna N.W., Payne S.M., Runyen-Janecky L.J., Zhou S., RA Schwartz D.C., Blattner F.R., RT "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T"; RL Infect. Immun. 71:2775-2776 (2003). RN [5]
9	30	88.2	80	1 POC7_CYND	
10	30	88.2	81	1 POC3_SYRVO	
11	30	88.2	81	1 POC3_OLEEU	
12	30	88.2	85	1 POC4_ALNGU	
13	30	88.2	85	1 POC4_BETVE	
14	30	88.2	148	1 CALL_DROME	
15	30	88.2	148	1 CALM_METSER	
16	30	88.2	148	1 CALM_PATESP	
17	30	88.2	214	1 HS30_ONCITS	
18	30	88.2	259	1 FKB7_HUMAN	
19	30	88.2	311	1 RCN1_HUMAN	
20	30	88.2	340	1 YMDF7_YEAST	
21	30	88.2	389	1 TAL_GLOVI	
22	30	88.2	391	1 TAL_SYN3	
23	30	88.2	402	1 PGH1_ERMCIA	
24	30	88.2	402	1 PGH2_ERMCIA	
25	30	88.2	433	1 HTR2_HALVA	
26	30	88.2	438	1 POHO_PSPAE	
27	30	88.2	444	1 GID_STRR6	
28	30	88.2	468	1 AMFB_BACFI	
29	30	88.2	472	1 RE16_SCHPO	
30	30	88.2	477	1 FES_FSVST	
31	30	88.2	494	1 TCN1_STRGA	
32	30	88.2	529	1 HSF1_HUMAN	
33	30	88.2	559	1 PMGI_MAIZE	

Scoring table: BL2USM62
Gapop 10.0 , Gapext 0.5
Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries
Database : Swissprot_42:*

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description	SEQUENCE FROM N.A.
1	34	100.0	325	1 UP14_ECOLI	SPECIES=E.coli; STRAIN=K12 / MG1655; RC MEDLINE=9426617; PubMed=9278503;
2	34	100.0	763	1 HTR2_HALSA	RA Blattner R.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V., RA Riley M., Collado-Vides J., Glasner J.D., Rose C.K., Mayhew G.F., RA Gregor J.J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., RA Mau B., Shao Y.; RT "The complete genome sequence of Escherichia coli K-12."; RN [1]
3	34	100.0	764	1 HTR2_HALSA	RC SEQUENCE OF 1-12. RX MEDLINE=7443975; PubMed=9288646; RN [2]
4	34	100.0	778	1 HTR6_HALSA	RA Link A.J., Robison K., Church G.M.; RT "Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12."; RL Electrophoresis 18:1259-1313 (1997). RN [3]
5	34	100.0	778	1 HTR6_HALSA	RC SEQUENCE FROM N.A. SPECIES=S.flexneri; STRAIN=301 / Serotype 2a; RC MEDLINE=22406; PubMed=12384530;
6	31	91.2	535	1 HTR1_HALSA	RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y., RA Yu J.; RT "Genome sequence of shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157:H7"; RL Nucleic Acids Res. 30:4432-4441 (2002). RN [4]
7	31	91.2	535	1 HTR1_HALSA	RC SEQUENCE FROM N.A. SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a; RC MEDLINE=2259074; PubMed=12704152;
8	30	88.2	78	1 POC7_PHLPR	RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., RA Fournier G., Mayhew G.P., Plunkett G., III, Rose D.J., Darling A., RA Mau B., Perna N.W., Payne S.M., Runyen-Janecky L.J., Zhou S., RA Schwartz D.C., Blattner F.R., RT "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T"; RL Infect. Immun. 71:2775-2776 (2003). RN [5]
9	30	88.2	80	1 POC7_CYND	
10	30	88.2	81	1 POC3_SYRVO	
11	30	88.2	81	1 POC3_OLEEU	
12	30	88.2	85	1 POC4_ALNGU	
13	30	88.2	85	1 POC4_BETVE	
14	30	88.2	148	1 CALL_DROME	
15	30	88.2	148	1 CALM_METSER	
16	30	88.2	148	1 CALM_PATESP	
17	30	88.2	214	1 HS30_ONCITS	
18	30	88.2	259	1 FKB7_HUMAN	
19	30	88.2	311	1 RCN1_HUMAN	
20	30	88.2	340	1 YMDF7_YEAST	
21	30	88.2	389	1 TAL_GLOVI	
22	30	88.2	391	1 TAL_SYN3	
23	30	88.2	402	1 PGH1_ERMCIA	
24	30	88.2	402	1 PGH2_ERMCIA	
25	30	88.2	433	1 HTR2_HALVA	
26	30	88.2	438	1 POHO_PSPAE	
27	30	88.2	444	1 GID_STRR6	
28	30	88.2	468	1 AMFB_BACFI	
29	30	88.2	472	1 RE16_SCHPO	
30	30	88.2	477	1 FES_FSVST	
31	30	88.2	494	1 TCN1_STRGA	
32	30	88.2	529	1 HSF1_HUMAN	
33	30	88.2	559	1 PMGI_MAIZE	

-!- SIMILARITY: Contains 2 HAMP domains.

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CC EMBL; X95590; CAA61843.1; -.

DR PIR; T48897; T48897.

DR HSSP; P03942; 1QUT.

DR InterPro; IPR004089; Chmtaxis_transd.

DR InterPro; IPR003660; HAMP.

DR InterPro; IPR004090; Me_chemotaxis.

DR Pfam; PF00672; HAMP; 1.

DR PRINTS; PR00260; CHEMTRNSDUCR.

DR SMART; SM00304; HAMP; 2.

DR PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.

DR PROSITE; PS50885; HAMP; 2.

KW Transducer; Transmembrane; Repeat.

FT DOMAIN 1 26 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 27 47 POTENTIAL.

FT DOMAIN 48 296 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 297 317 POTENTIAL.

FT DOMAIN 318 778 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 318 370 HAMP 1.

FT DOMAIN 412 465 HAMP 2.

FT DOMAIN 484 720 METHYL.ACCEPTING TRANSDUCER.

FT DOMAIN 778 AA; 82077 MW; 134CD7F0A3334CD CR664;

SQ Query Match 100.0%; Score 34; DB 1; Length 778;

Best Local Similarity 100.0%; Pred. No. 44;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGDGFA 6

Db 617 DGDGFA 622

RESULT 6

HPRL_HALNI STANDARD; PRT; 535 AA.

AC P33741; Q9HPFG6 (Rel. 28, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DB Sensory rhodopsin I Transducer (HTR-I) (Methyl-accepting phototaxis protein I) (MPP-I).

GN HTRI OR HTRI OR VNGI659G.

O9 Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081), and

OC Archaea; Buryarchaeota; Halobacteria; Halobacteriales;

OC Halobacteriaceae; Halobacterium.

OX NCBI_TaxID=64091, 2242;

RN [1]

SEQUENCE FROM N.A.

STRAIN=NRC-1;

RX MEDLINE=20504483; PubMed=11016950;

RA NG W.V., Kennedy S.P., Mahaivas G.G., Berquist B., Pan M., Thorquist V., Shirogna J., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartz S., Weir D., Hall J., Dahl T.A., Walti R., Goo Y.A., Leithauer B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenburger T.A., Peck R.F., Pohlischroder J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebbhardt H., Low T.M., Liang P., Riley M., Hood L., Dassarma S.; RT "Genome sequence of Halobacterium species NRC-1"; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000). [2]

RP SEQUENCE FROM N.A.; AND SEQUENCE OF 1-10; 350-377 AND 457-476.

RC SPECIES_H.halobium; STRAIN=FLX5R;

RA MEDLINE=93101637; PubMed=1465418;

RA "Primary structure of an archaeabacterial transducer, a methyl-accepting protein associated with rhodopsin I.";

RT Proc. Natl. Acad. Sci. U.S.A. 89:11915-11919 (1992).

RL !- FUNCTION: TRANSDUCES SIGNALS FROM THE PHOTOTAXIS RECEPTOR TO THE FLAGELLAR MOTOR. RESPONDS TO SENSORY RHODOPSIN I (SR-I) LIGHT CHANGES THROUGH THE VARIATION OF THE LEVEL OF METHYLATION.

CC !- SIMILARITY: Contains 1 methyl-accepting transducer domain.

CC !- SIMILARITY: Contains 2 HAMP domains.

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CC EMBL; AB005075; AAC19913.1; -.

DR EMBL; L05603; AA7215.1; -.

DR PIR; A47190; AA7215.1; -.

DR E84318; E84318.

DR HSSP; P02942; 1077.

DR InterPro; IPR004089; Chmtaxis_transd.

DR InterPro; IPR003660; HAMP.

DR InterPro; IPR004090; Me_chemotaxis.

DR Pfam; PF00672; HAMP; 1.

DR Pfam; PF00015; MCPsignal; 1.

DR PRINTS; PR00260; CHEMTRNSDUCR.

DR SMART; SM00304; HAMP; 2.

DR SMART; SM00383; MA; 1.

DR PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.

DR PROSITE; PS50885; HAMP; 2.

KW Transducer; Photoreceptor; Transmembrane; Methylation; Complete proteome; Repeat.

FT INIT MET 0 0 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 1 13 POTENTIAL.

FT TRANSMEM 14 28 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 29 38 POTENTIAL.

FT TRANSMEM 39 54 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 55 535 HAMP 1.

FT DOMAIN 54 106 HAMP 2.

FT DOMAIN 148 201 HAMP 2.

FT DOMAIN 220 458 METHYL-ACCEPTING TRANSDUCER.

FT MOD_RES 265 METHYLATION.

FT MOD_RES 272 272 METHYLATION.

FT MOD_RES 279 279 METHYLATION.

FT MOD_RES 463 463 METHYLATION.

FT MOD_RES 472 472 METHYLATION.

FT SEQUENCE 535 AA; 5654 MW; B9945BE4F66A9B091 CRC64/

Query Match 91.12%; Score 31; DB 1; Length 535;

Best Local Similarity 83.3%; Pred. No. 1.1e-02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGDGFA 6

Db 355 DGDGFS 360

RESULT 7

HTRI_HALSA STANDARD; PRT; 535 AA.

ID P33955; AC P33955; DT 01-FEB-1994 (Rel. 28, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Sensory rhodopsin I transducer (HTR-I) (Methyl-accepting phototaxis protein I) (MPP-I).

GN HTRI OR HTRI OR VNGI659G.

O9 Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081), and

OC Archaea; Buryarchaeota; Halobacteria; Halobacteriales;

OC Halobacteriaceae; Halobacterium.

OX NCBI_TaxID=64091, 2242;

RN [1]

SEQUENCE FROM N.A.

STRAIN=NRC-1;

RX MEDLINE=20504483; PubMed=11016950;

RA NG W.V., Kennedy S.P., Mahaivas G.G., Berquist B., Pan M., Thorquist V., Shirogna J., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartz S., Weir D., Hall J., Dahl T.A., Walti R., Goo Y.A., Leithauer B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenburger T.A., Peck R.F., Pohlischroder J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebbhardt H., Low T.M., Liang P., Riley M., Hood L., Dassarma S.; RT "Genome sequence of Halobacterium species NRC-1"; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000). [2]

OS Halobacterium salinarium.
 CC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TAXID=2242;
 RN [1] _____.
 RP SEQUENCE FROM N.A.
 RC STRAIN=L3; PubMed=2205842;
 RX MEDLINE=90184855; PubMed=2205842;
 RA Ferrando E., Krah M., Marwan W.; Oesterhelt D.;
 RT "A gene from *S. pombe* with homology to *E. coli* RNAse III blocks
 RT conjugation and sporulation when overexpressed in wild type cells.";
 RL Nucleic Acids Res. 18:5304-5304(1990).
 RN [2] _____.
 RP FUNCTION.
 RX MEDLINE=94244615; PubMed=8187768;

RA Krah M., Marwan W., Vermeglio A., Oesterhelt D.;
 RT "Phototaxis of Halobacterium salinarium requires a signalling complex
 of sensory rhodopsin I and its methyl-accepting transducer HtrI.";
 RL J. 13:2150-2155(1994).
 CC !- FUNCTION: TRANSDUCES SIGNALS FROM THE PHOTOTAXIS RECEPTOR
 CC SENSORY RHODOPSIN I (SR-I) TO THE FLAGELLAR MOTOR. RESPONDS TO
 CC LIGHT CHANGES THROUGH THE VARIATION OF THE LEVEL OF METHYLATION.
 CC !- SIMILARITY: Contains 1 methyl-accepting transducer domain.
 CC !- SIMILARITY: Contains 2 HAMP domains.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; X68591; CAA8578.1; -.
 DR HSSP; P02942; IQU7.
 DR InterPro; IPRO004089; Chmtaxis_transd.
 DR InterPro; IPRO03660; HAMP.
 DR InterPro; IPRO04050; Me_chemotaxis.
 DR Pfam; PF00672; HAMP; 1.
 DR PRINTS; PR00015; MCP1ignal; 1.
 DR PRINTS; PR00260; CHEMTNSDUR.
 DR SMART; SM00304; HAMP; 2.
 DR PROSITE; PS00283; MA; 1.
 DR PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
 KW Transducer; Photoreceptor; Transmembrane; Methylation; Repeat.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 9 29 POTENTIAL.
 FT DOMAIN 30 33 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 34 54 POTENTIAL.
 FT DOMAIN 55 535 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 54 106 HAMP 1.
 FT DOMAIN 148 201 HAMP 2.
 FT MOD_RES 220 458 METHYL-ACCEPTING TRANSDUCER.
 FT MOD_RES 265 265 METHYLATION (BY SIMILARITY).
 FT MOD_RES 272 272 METHYLATION (BY SIMILARITY).
 FT MOD_RES 279 279 METHYLATION (BY SIMILARITY).
 FT MOD_RES 463 463 METHYLATION (BY SIMILARITY).
 FT MOD_RES 472 472 METHYLATION (BY SIMILARITY).
 SQ 535 AA; 56814 MW; 504A165A4/FABA45 CRC64;

Query Match Score 31; DB 1; Length 535;
 Best Local Similarity 91.2%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGDGF 6
 Db 355 DGDGF 360

RESULT 8
 POC7_PHLPR

SEQUENCE FROM N.A.

RC TISSUE=Pollen;

OS Halobacterium salinarium.
 CC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TAXID=2242;
 RN [1] _____.
 RP SEQUENCE FROM N.A.
 RC STRAIN=L3; PubMed=2205842;
 RX MEDLINE=90184855; PubMed=2205842;
 RA Ferrando E., Krah M., Marwan W.; Oesterhelt D.;
 RT "A gene from *S. pombe* with homology to *E. coli* RNAse III blocks
 RT conjugation and sporulation when overexpressed in wild type cells.";
 RL Nucleic Acids Res. 18:5304-5304(1990).
 RN [2] _____.
 RP FUNCTION.
 RX MEDLINE=94244615; PubMed=8187768;
 RA Krah M., Marwan W., Vermeglio A., Oesterhelt D.;
 RT "Phototaxis of Halobacterium salinarium requires a signalling complex
 of sensory rhodopsin I and its methyl-accepting transducer HtrI.";
 RL J. 13:2150-2155(1994).
 CC !- FUNCTION: TRANSDUCES SIGNALS FROM THE PHOTOTAXIS RECEPTOR
 CC SENSORY RHODOPSIN I (SR-I) TO THE FLAGELLAR MOTOR. RESPONDS TO
 CC LIGHT CHANGES THROUGH THE VARIATION OF THE LEVEL OF METHYLATION.
 CC !- SIMILARITY: Contains 1 methyl-accepting transducer domain.
 CC !- SIMILARITY: Contains 2 HAMP domains.

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DR EMBL; Y17835; CAA76887.1; -.
 DR HSSP; P25070; IAVU.
 DR InterPro; IP000248; EF-hand.
 DR InterPro; IPRO0115; Recoverin.
 DR PRINTS; PR00036; ethand; 2.
 DR PRINTS; PR000450; RECOVERIN.
 DR ProDom; PD00012; EF-hand; 1.
 DR SMART; SM00054; EFh; 2.
 DR PROSITE; PS00018; EF HAND; 2.
 KW Calcium binding; Repeat; Allosteric.
 FT CA_BIND 13 24 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 48 59 EF-HAND 2 (POTENTIAL).
 SQ SEQUENCE 78 AA; 8677 MW; 1469370AAE2244 CRC64;

Query Match Score 30; DB 1; Length 78;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGDGF 5
 Db 50 DGDGF 54

RESULT 9
 POC7_CYNDA

ID POC7_CYNDA STANDARD; PRT; 80 AA.
 AC B94052; Q9SAR4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Polyclinic Cyn d 7 (Calcium-binding pollen allergen Cyn d 7) (Calcium
 DE bind protein B1).
 OS Cynodon dactylon (Bermuda grass).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCD clade; Chloridoideae; Cyperaceae; Cyndoneae.
 OX NCBI_TAXID=28909;
 RN [1] _____.
 RP SEQUENCE FROM N.A.

MEDLINE=97188603; PubMed=9037188;
 RX RA Suphioglu C.; Ferreira F.; Knox R.B.;
 RT "Molecular cloning and immunological characterisation of Cyn d 7, a
 novel calcium-binding allergen from Bermuda grass pollen.";
 RT PEBS Lett. 402:167-172(1997).
 RL [2]
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pollen;
 MEDLINE=9802858; PubMed=9363908;
 RX RA Smith P.M.; Xu H.; Swoboda I.; Singh M.B.;
 RT "Identification of a Ca²⁺-binding protein as a new Bermuda grass
 pollen allergen Cyn d 7: IgE cross-reactivity with oilseed rape
 pollen allergen Bra r 1.";
 RT Int. Arch. Allergy Immunol. 114:265-271(1997).
 RL [2]
 CC -!- ALLEGGEN: Causes an allergic reaction in human. Binds IgE.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 CC
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 CC
 DR EMBL; X91266; CAA6234.1; ALT INIT.
 DR EMBL; U35683; AAC4964.1; ALT_INIT.
 DR EMBL; U75585; AAD00247.1; -.
 HSSP; P25070; IAVS.
 InterPro; IPR02048; EF-hand.
 Pfam; PF00036; e�hand; 2.
 PRODOM; PD00012; EF-hand; 1.
 SMART; SM00054; EFH; 2.
 PROSITE; PS00018; EF HAND; 2.
 Calcium-binding; Repeat; Allergen.
 CA_BIND 15 26 EF-HAND 1 (POTENTIAL).
 CA_BIND 50 61 EF-HAND 2 (POTENTIAL).
 FT F83347BD7C2676F5 CRC64;
 SQ SEQUENCE 80 AA; 8801 MW;
 Query Match 88.2%; Score 30; DB 1; Length 80;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OX
 DR EMBL; AF078681; AAC01144.1; -.
 DR HSSP; P02588; IAVS.
 InterPro; IPR02048; EF-hand.
 Pfam; PF00036; e�hand; 2.
 PRODOM; PD000012; EF-hand; 1.
 SMART; SM00054; EFH; 2.
 PROSITE; PS00018; EF HAND; 2.
 Calcium-binding; Repeat; Allergen.
 CA_BIND 16 27 EF-HAND 1 (POTENTIAL).
 CA_BIND 51 62 EF-HAND 2 (POTENTIAL).
 FT CA_BIND 81 AA; 8994 MW;
 SQ 9C0CA8BCEB03B37A CRC64;
 Query Match 88.2%; Score 30; DB 1; Length 81;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 POC3_OLEEU
 ID POC3_OLEEU
 AC 081052;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Polcalcin Ole e 3 (Calcium-binding pollen allergen Ole e 3).
 GN OLE3.
 Olea europaea (Common olive).
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Oleaceae; Olea.
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Oleaceae; Olea.
 RN NCBI_TaxID=4146;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pollen; PubMed=9874211;
 RX MBLJINE=99089607; PubMed=9874211;
 RA Ledesma A.; Villalba M.; Batanero E.; Rodriguez R.;
 RT "Molecular cloning and expression of active Ole e 3, a major allergen
 from olive-tree pollen and member of a novel family of Ca2+-binding
 proteins (polcalcins) involved in allergy.";
 RT Bur. J. Biochem. 258:454-459(1998).
 RL
 CC -!- ALLERGEN: Causes an allergic reaction in human. Binds IgE.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF015810; AAD05375.1; -.
 DR HSSP; P02588; IAVS.
 InterPro; IPR02048; EF-hand.
 Pfam; PF00036; e�hand; 2.
 PRODOM; PD000012; EF-hand; 1.
 SMART; SM00054; EFH; 2.
 PROSITE; PS00018; EF HAND; 2.
 Calcium-binding; Repeat; Allergen.
 KW
 FT CA_BIND 19 30 EF-HAND 1 (POTENTIAL).
 CA_BIND 54 65 EF-HAND 2 (POTENTIAL).
 SQ BC3B3DDE011D409D0 CRC64;
 Sequence 84 AA; 9356 MW;

RESULT 10
 POC3_SYRVU
 ID POC3_SYRVU
 AC P58711;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE SYRV3.
 GN Syringa vulgaris (Common lilac).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Oleaceae; Syringa.
 OX NCBI_TaxID=34270;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pollen; Villalba M.; Rodriguez R.;
 RA Ledesma A.; Villalba M.; Rodriguez R.;
 RT "Cloning and expression of a protein homologous to Ole e 3 from
 Syringa vulgaris.";
 Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 BL -!- ALLEGGEN: Causes an allergic reaction in human.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 CC
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Query Match	Best Local Similarity	Score	DB 1;	Length
Matches 5 ; Conservative	88.2% ; 100.0%	30; Pred. No. 27;	84;	
	Mismatches 0;	Mismatches 0;	0;	Indels
1	DGDFP 5			
56	DGDGF 60			

Polcalcin Bet v 4 (calcium-binding pollen allergen Bet v 4).
BetV4.
Betula verrucosa (White birch) (*Betula pendula*).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop-
spermatozophyta; Magnoliophyta; eudicotyledons; core eudicots;
eucommias; Fagales; Betulaceae; *Betula*.
NCBI TaxID: 3500;
BETV4.

SUULT 1.2
C4_ALNGL
POC ALNGL
081761
STANDARD;
PRT;
85 AA.

ISSUE=Polien;
MEDILINE=P-8019240; PubMed=9353329;
Engel E., Richter K., Obermeyer G., Brizza P., Kungl A.J., Sir Auer M., Böner C., Rheinberger H.J., Brittenbach M., Ferreira "Immunochemical and biological properties of Bet v 4, a novel pollen allergen with two EF-hand calcium-binding domains." J. Biol. Chem. 72:28630-28637(1997).

Alnus glutinosa (L.) S. Baum binding pollen allergen Aln g 4.
Alnus glutinosa (Alder).
Bukaryota; *Viridiplantae*; *Streptophyta*; *Embryophyta*; *Tracheophyta*; *Spermatophyta*; *Magnoliophyta*; *eudicots*; *eucommiids*; *core eudicots*; *rosids*; *eurosid s I*; *Fagales*; *Betulaceae*; *Alnus*.
 NCBI_TAXID=3517;
 [1]
 SEQUENCE FROM N.A., AND CHARACTERIZATION.
 TISSUE=PODULE;
 TISSUE=PODULE;
 MEDLINE=99075756; PubMed=9862740;
 Hayek B., Vangelista L., Pastore A., Sperr W.R., Valent P., Vrtala S., Niederberger V., Twarodosz A., Kraft D., Valent A.R.; "Molecular and immunologic characterization of a highly cross-reactive two EF-hand calcium-binding alder pollen allergen, Aln g 4: structural basis for calcium-modulated IgE recognition." J. Immunol. 161:7031-7039 (1998).

SEQUENCE FROM N. A.
TISSUE=POLLEN;
MEDLINE=8005106; PubMed=9345295;
Twardosz A., Hayek B., Seiberler S., Pastore A., Vangelista L.,
Groenlund H., Kraft D., Valenta R.;
Molecular characterization, expression in Escherichia coli,
epitope analysis of a two EF-hand calcium-binding birch pollen
allergen. Ref. "A".

- ! MASS SPECTROMETRY: MW 9318.6; METHOD: MALDI.
- ! ALLERGEN: causes an allergic reaction in human.
- ! SIMILARITY: Contains 2 EF-hand calcium-binding domains.

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PRODOM; P0000012; EF-hand; 1.
SMART; SM00054; EFHand; 2.
PROSITE; PS00018; EF HAND; 2.
Calcium-binding; Repeat; Allergen.

CA_BND 55 66
CONFICT 71 71
SEQUENCE 85 AA; 9447 MW;

```

1 DGDFP 5
||| |
52 DCDG 6

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ULT 13
4 BETVE
POC4_BETVE_STANDARD; PRT;
Q39419; 004131;
16-OCT-2001 (Rev. 40, Created)
16-OCT-2001 (Rev. 40, Last sequence update)
10-OCT-2003 (Rev. 42, Last amendment)
57 DGDGF 61

T 14	DROME CALL9258;	STANDARD; PRT;	148 AA.
	Q9VBLS9; 01-FEB-1996 (Rel. 33, Created)		
	0110-OCT-2003 (Rel. 42, Last sequence update)		
	Calmodulin related procain 9TA (Androcum protein).		
	Drosophila melanogaster (Fruit fly).		

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydriidae; Drosophilidae; Drosophila.
[1] NCBI_TaxID=727;

SEQUENCE FROM N.A.;
MEDLINE=0571221; PubMed=7980384;
RX Parker H., Hutchinson B., Fyrberg E.A.;
RA "Drosophila melanogaster genes encoding three trponin-C isoforms and
a calmodulin-related protein";
RT Biochem. Genet. 32:119-135(1994).
[2]

SEQUENCE FROM N.A.;
STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
RX Adams M.D., Celminier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.Y., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.S., Champé M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Miklos G.I.G.,
RA Abril J.F., Agadjanyan A.H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandaari D., Bolishakov S.,
RA Borckova D., Borchtein P., Brottier P.,
RA Burtsis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davempt L.B., Davies P.,
RA Cherie P.B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doupe L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferreria S., Fleischmann W.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hwang D., Howland T.J., Ibeagwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchem K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Moriarity C., Morris J., Mosnerei A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Neilson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puriv V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of *Drosophila melanogaster*";
RT Science 287:2185-2195(2000).

RL FUNCTION: May be involved in calcium-mediated signal transduction.

CC - SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS

CC - FUNCTION: To other EF-hand calcium binding proteins

CC - SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS

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CC or send an email to license@isb-sib.ch).

CC EMBL; X76045; CAA53630.1; -.

CC HSSP; P02593; 1FWA4.

CC FlyBase; FBgn0011273; And.

GO; GO:0005634; C:cytoplasm; IDA.

DR InterPro; IPR002048; EF-hand.

DR Pfam; PF00036; eHand; 4.

DR ProDom; PD00012; EF-hand; 2.

DR SMART; SM00054; EFh; 4.

Query Match 88.2%; Score 30; DB 1; Length 148;

Best Local Similarity 100.0%; Pred. No. 48;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Wed Jun 2 16:48:17 2004

us-09-715-763a-5.rsp

Page 9

Qy 1 DGDGF 5
| |||
Db 95 DGDGF 99

Search completed: June 1, 2004, 18:09:01
Job time : 12 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2004, 18:05:23 ; Search time 39 Seconds

(without alignments)
48.541 Million cell updates/sec

Title: US-09-715-763A-5

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archeap:*

17 34 100.0 627 17 Q9HS86 halobacteri
18 34 100.0 777 1 P71415
19 34 100.0 788 1 Q93643
20 34 100.0 789 17 Q9HRA1
21 34 100.0 948 16 Q8XX42
22 34 100.0 985 16 Q8XUP9 ralstonia s
23 34 100.0 1351 16 Q8XZ58 ralstonia s
24 34 100.0 3770 16 Q87G75 vibrio para
25 31 91.2 133 7 Q860H6 gallus gall
26 31 91.2 195 10 Q84Y42 ranunculus
27 31 91.2 233 2 Q9L3F3
28 31 91.2 262 12 Q89340 paramecium
29 31 91.2 267 16 Q9HZ01 pseudomonas
30 31 91.2 279 2 Q8RJQ9 thauera aro
31 31 91.2 288 16 Q9n6P1 leishmania
32 31 91.2 288 16 Q8CPF2 staphylococ
33 31 91.2 347 17 Q97BL3 thermoplasm
34 31 91.2 353 16 Q89V56 bradyrhizob
35 31 91.2 372 7 Q31406 gallus gall
36 31 91.2 374 5 Q9N6B1
37 31 91.2 433 16 Q92TA1
38 31 91.2 475 16 Q82CQ6 streptomyce
39 31 91.2 481 16 Q82EY7
40 31 91.2 486 5 Q8SYF5 drosophila
41 31 91.2 489 16 Q82NZ1 streptomyce
42 31 91.2 532 16 Q9L1U5 leptospira
43 31 91.2 560 16 Q8FA15
44 31 91.2 576 16 Q9L1L5 streptomyce
45 31 91.2 635 2 Q84HK0 streptomyce

ALIGNMENTS

RESULT 1
Q8EY42 PRELIMINARY ; PRT; 230 AA.

ID Q8EY42 ; PRELIMINARY ; PRT; 230 AA.
AC Q8EY42 ;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DR 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DR 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Two-component response regulator.
GN LB015.
OS Leptospira interrogans .
OC Spirochaetes ; Spirochaetales ; Leptospiraceae ; Leptospira .
RN [1] _TaxID=173 ; InterPro; IPR001867 ; Trans-reg_C .
RN [1] _SEQUENCE FROM N_A .
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai ;
RA Ren S ; Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases .
RL EMBL; AS011590; AAN51574.1; - ; DR GO; GO:0000156; F: two-component response regulator activity; IEA. .
DR GO:0003677; F: DNA binding; IEA. .
DR GO:0000160; P: two-component signal transduction system (p. . . ; IEA. .
DR InterPro; IPR001749 ; Trans-reg_C .
DR InterPro; IPR001867 ; Trans-reg_C .
DR Pfam; PF00072; response_reg_C; 1. .
DR Pfam; PF0486; trans_reg_C; 1. .
DR ProDom; PD000039; Response reg; 1. .
DR ProDom; PD000329; Trans_reg_C; 1. .
DR SMART; SM00448; RBC; 1. .
DR PROSITE; PS50110; RESPONSE_REGULATOR; 1. .
DR Complete proteome .
SQ Sequence 230 AA; 26523 MW; OC5949D2E28E6AE CRC64 ;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	34	100.0	230	16	Q8EY42		Q8EY42 leptospira
2	34	100.0	273	16	Q25312		Q25312 helicobacte
3	34	100.0	273	16	Q9ZLP0		Q9ZLP0 helicobacte
4	34	100.0	274	2	Q68229		Q68229 helicobacte
5	34	100.0	276	1	Q9P9a7		Q9P9a7 uncultured
6	34	100.0	288	16	Q9RB6		Q9RB6 bacillus ha
7	34	100.0	288	16	Q8WQ9		Q8WQ9 bacillus ha
8	34	100.0	288	16	Q8IA22		Q8IA22 bacillus ce
9	34	100.0	310	16	Q98FP0		Q98FP0 rhizobium m
10	34	100.0	310	16	Q92v50		Q92v50 rhizobium m
11	34	100.0	310	16	Q9X7X2		Q9X7X2 streptomyce
12	34	100.0	325	16	Q8UCN0		Q8UCN0 agrobacteri
13	34	100.0	326	16	Q8KD41		Q8KD41 escherichia
14	34	100.0	326	16	Q8FF70		Q8FF70 escherichia
15	34	100.0	536	17	Q9HPA2		Q9HPA2 halobacteri
16	34	100.0	539	10	Q7xx03		Q7xx03 oryza sativ

Query Match 100.0% ; Best Local Similarity 100.0% ; Matches 6 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

QY 1 DGDGFA 6

DG 5B DGDGFA 63

SQ	SEQUENCE	273 AA;	30429 MW;	A9A9BEB5D4DB634E CRC64;
RESULT 2				
ID O25312	PRELIMINARY;	PRT;	273 AA.	
AC Q25312;				
DT 01-JAN-1998	(TREMBLrel. 05; Created)			
DR 01-JAN-1998	(TREMBLrel. 05; Last sequence update)			
DT 01-JUN-2003	(TREMBLrel. 24; Last annotation update)			
DE Ferredoxin oxidoreductase, beta subunit.				
GN HP0590.				
OS Helicobacter pylori (Campylobacter pylori).				
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;				
OC Helicobacteraceae; Helicobacter.				
OX NCBI_TAXID=210;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=26700 / ATCC 700392;				
RX MEDLINE=97394467; PubMed=952185;				
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Sutton G.G., Gill S., Dougherty B.A., Gill S., Dougherty B.A.,				
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,				
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Peterson S.,				
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., Glodek A.,				
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., Glodek A.,				
RA McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Hickey E.K.,				
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Kelley J.M.,				
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E., Wallin E.,				
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.,				
RA "The complete genome sequence of the gastric pathogen Helicobacter pylori.";				
RT Nature 388:539-547(1997).				
RT EMBL; AE000572; AAD07655.1; -.				
DR PIR; F64593; F64593.				
DR TIGR; HP0590; -.				
KW Hypothetical protein; Complete proteome;				
SQ SEQUENCE 273 AA;	30414 MW;	F3FD181BAE32AB CRC64;		
Query Match Score 34; DB 16; Length 273;				
Best Local Similarity 100.0%; Pred. No. 1.2e+02;				
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY 1 DGDDFA 6				
Db 95 DGDDFA 100				
RESULT 3				
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ID O9ZLPO;				
AC Q9ZLPO;				
DT 01-MAY-1999	(TREMBLrel. 10; Created)			
DT 01-MAY-1999	(TREMBLrel. 10; Last sequence update)			
DT 01-JUN-2003	(TREMBLrel. 24; Last annotation update)			
DE Subunit of 2-oxoglutarate oxidoreductase.				
GN O9B OR JHP0538.				
OS Helicobacter pylori J99 (Campylobacter pylori J99).				
OC Helicobacteraceae; Helicobacter.				
OC Helicobacteraceae; Helicobacter.				
OX NCBI_TAXID=85963;				
RN [1]				
RP SEQUENCE FROM N.A.				
RX MEDLINE=99120557; PubMed=9923682;				
RA Alm R.A., Ling L.-S.T., Moir D.B.T., King B.L., Brown B.D., Doig P.C.,				
RA Smith D.R., Noontan B., Guild B.C., de Jonge B.L., Carmel G., Ires C.,				
RA Tummino P.J., Caruso A., Urias-Nickelsen M., Mills D.M., Mills D.M., Vovis G.F.,				
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,				
RA Trussell T.J.;				
RA "Genomic sequence comparison of two unrelated isolates of the human Gastric pathogen Helicobacter pylori."				
BL Nature 397:176-180(1999).				
DR AEP01486; AAD06120.1; -.				
DR Commire proteome				
RN [1]				
RP SEQUENCE FROM N.A.				
RX MEDLINE=21128653; PubMed=11233160;				
RA Beja O., Suzuki M.T., Koornin E.V., Aravind L., Hadd A., Nguyen L.P.,				
RA Villacorta R., Amjadi M., Garrigues C., Jovanovich S.B., Feldman R.A.,				
RA Delong E.F.,				
RT "Construction and analysis of bacterial artificial chromosome libraries from a marine microbial assemblage."				
RT Libraries				

OX NCBI_TAXID=381;				
[1] SEQUENCE FROM N.A.				
RP STRAIN=MAFFE03059;				
RC MEDLINE=21082930; PubMed=11214968;				
RX KANEKO T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,				
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,				
RA Kishida Y., Kiyokawa C., Kohara M., Matsunoto M., Matsuno A.,				
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpou S., Sugimoto M.,				
RA Takeuchi C., Yamada M., Tabata S.;				
RT "Complete genome sequence of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti";				
RL DNA Res. 7:331-338 (2000).				
DR EMBL; AP003002; BAB50527.1; -.				
DR InterPro; IPR043360; Gly_bleo_diox.				
DR Pfam; PF00903; Glyoxalase; 1.				
KW Complete proteome.				
SQ SEQUENCE 310 AA; 34199 MW; 2345BBEBC59FF390 CRC64;				
Query Match 100.0%; Score 34; DB 16; Length 310;				
Best Local Similarity 100.0%; Pred. No. 1.4e+02;				
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
RESUL 10				
Q92V50 PRELIMINARY; PRT; 310 AA.				
ID Q92V50; AC 01-DEC-2001 (TREMBLrel. 19, Created)				
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
DB Hypothetical protein RB0867.				
GN SRSB2 OR SRSB102.				
OS Rhizobium meliloti (Sinorhizobium meliloti).				
OG Plasmid pSymb (megaplasmid 2).				
OC Rhizobiaceae; Proteobacteria; Alphaproteobacteria; Rhizobiales;				
OC Sinorhizobium/Ensifer group; Sinorhizobium.				
NCBI_TAXID=382;				
RN SEQUENCE FROM N.A.				
RP STRAIN=1021;				
RX MEDLINE=21396508; PubMed=11481431;				
RA Finan T.M., Weidner S., Wong K., Bahrmeister J., Chain P.,				
RA Vorhoelter P.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,				
RA Golding B., Puehler A.;				
RT "The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti.";				
RL EMBL; AL601645; CAC42267.1; -.				
DR PIR; C95950. GO; GO:004621; C:extrachromosomal DNA; IEA.				
DR InterPro; IPR043360; Gly_bleo_diox.				
DR Pfam; PF00903; Glyoxalase; 2.				
KW Plasmid; Hypothetical protein; Complete proteome.				
SQ SEQUENCE 310 AA; 34289 MW; 0DAC969D8DD3ADE CRC64;				
Query Match 100.0%; Score 34; DB 16; Length 310;				
Best Local Similarity 100.0%; Pred. No. 1.4e+02;				
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
RESULT 12				
O9X7X2 PRELIMINARY; PRT; 325 AA.				
Db 1 DGDGFA 6				
Db 123 DGDGFA 128				
RESUL 11				
O9X7X2 PRELIMINARY; PRT; 310 AA.				
Db 1 Q9X7X2				
AC ID ATU2453 OR AGR_C_4455.				
AC DE Aromatic compounds dioxygenase.				
AC GN SC06777 OR SC6A5_26C.				
OS Streptomyces coelicolor.				
OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;				
OC Streptomyicinae; Streptomyctaceae; Streptomyces.				
OX NCBI_TAXID=1902;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=A3 (2);				
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.				
RN [3]				
RP SEQUENCE FROM N.A.				
RC STRAIN=A3 (2);				
RX MEDLINE=97000351; PubMed=8843436;				
RA Redenbach M., Kieser H.M., Denapaitre D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;				
RA "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3 (2) chromosome." RT Mol. Microbiol. 21:77-96(1996). RL				
RN [4]				
RP SEQUENCE FROM N.A.				
RC STRAIN=A3 (2) / M145; RX MEDLINE=21396410; PubMed=12000953; RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris H.M., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbow Nowitsch E., Rajandream M.A., Rutherford K., Rutledge S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wettorrek A., Woodward J., Barrell B.G., Parkhill J., Hopwood D.A.;				
RA "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3 (2)." RT Nature 417:141-147 (2002) DR EMBL; AL939129; CAB39710.1; -. DR PIR; T35417; T35417. DR GO; GO:00004289; F:subtilase activity; IEA. DR GO; GO:0000508; P:protein analysis and peptidolysis; IEA. DR InterPro; IPR01279; BlaCmase-like. DR InterPro; IPR000209; Peptidase_S8. DR PRO00753; lactamase_B; 1_pfam; PF00136; SUSTILASE_ASP; 1. DR PROSITE; PS00136; SUSTILASE_ASP; 1. DR Complete proteome. DR PROSITE; PS00136; SUSTILASE_ASP; 1. KW Sequence 310 AA; 34781 MW; EE6D457AA081711RC CRC64; SQ 100.0% Score 34; DB 16; Length 310; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY 1 DGDGFA 6				
Db 295 DGDGFA 300				

OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium; Agrobacterium group; Agrobacterium;
 OC NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2.1608350; PubMed=11743193;
 RA Okura V.W., Zhou Y., Chen L., Kaul R., Monks D.B., Kitajima J.P., Woo L.,
 RA Okura V.W., Zhou Y., Chen L., Wood G.R., Almeida N.F. Jr., Tobe T.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bove D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kuryavivin T., Levy R., Li M.-J., McClelland E., Hattori M., Shinagawa H.;
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krasnow W., Perry M.,
 RA Gordons-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-P., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens C58.";
 RT "The genome sequence of Agrobacterium tumefaciens;
 RT Agrobacterium tumefaciens C58.";
 RT Agrobacterium tumefaciens C58 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=11608351; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,
 RA Qurolo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Liu F.,
 RA Houmali R., Gordon J., Vaudin M., Tarchouk O., BPP A., Liu F.,
 RA Wollam C., Allinger M., Dougherty D., Scott C., Lappas C., Markez B.,
 RA Flanagan C., Crowell C., Gurson J., Lono C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58.";
 RT Agrobacterium tumefaciens (2001).
 DR EMBL; AE009193; AAU43441.1; ALT_INIT.
 DR EMBL; AE008159; AAK88190.1; -.
 DR PIR; AC2878; AC2878.
 DR PIR; E97654; E97654.
 DR GO:0016702; F:oxidoreductase activity, acting on single d. . . ; IEA.
 DR InterPro; IPR004360; Gly bleo diox.
 DR Pfam; PF00903; Glycocalyx; 1.
 KW DiOxygenase; Complete proteome.
 SQ SEQUENCE 325 AA; 35533 MW;
 Query Match Score 100.0%; Score 34; DB 16; Length 325;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DGDGFA 6
 DB 134 DGDGFA 139

RESULT 13
 ID Q8XD41 PRELIMINARY;
 AC Q8XD41; 2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Orf, hypothetical protein.
 GN YGFZ OR 24236 OR EC33770.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=2.074935; PubMed=11200551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

RW Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 RN Nature 409:529-533(2001).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=2.1156231; PubMed=11258796;
 RA Hayashi T., Makino E., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
 RT DNA Res. 8:11-22 (2001).
 DR EMBL; AE005520; AAC58036.1;
 DR EMBL; AP002563; BAB37133.1; -.
 DR PIR; B91100; B91100.
 DR PIR; F85945; F85945.
 GO; GO:0004047; F:aminomethyltransferase activity; IEA.
 DR InterPro; IPR006222; GCV_T.
 DR Pfam; PF01571; GCV_T.
 DR PIR; PF01571; GCV_T.
 KW Complete proteome_ 326 AA; 36058 MW;
 SQ SEQUENCE 326 AA;
 Query Match Score 100.0%; Score 34; DB 16; Length 326;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DGDGFA 6
 DB 78 DGDGFA 83

RESULT 14
 ID Q8FE70 PRELIMINARY;
 AC Q8FE70; 2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DR Hypothetical protein.
 GN YGFZ OR C3479.

OS Escherichia coli O6.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=217992;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O6_H1 / CFT073 / ATCC 700928;
 RX MEDLINE=2.2388234; PubMed=12471157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Rasko D., Buckles E.L., Liu S.-R., Boutin A., Hackett J., Strand D.,
 RA Mayhew G.F., Rose D.J., Zhou S.-R., Schwartz D.C., Perna N.T.,
 RA Mobiley R.I.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence of the uropathogenic Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
 DR EMBL; AE016766; AA81927.1;
 DR GO; GO:0004047; F:aminomethyltransferase activity; IEA.
 DR InterPro; IPR006222; GCV_T.
 DR Pfam; PF01571; GCV_T.
 DR Hypothetical protein; Complete proteome.
 SQ SEQUENCE 326 AA; 32658 MW;

Query Match Score 100.0%; Score 34; DB 16; Length 326;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGDGFA 6
 DB 78 DGDGFA 83

RESULT 15

C9HPA2	PRELIMINARY;	PRT;	536 AA.
ID Q9HPA2			
AC Q9HPA2;			
DT 01-MAR-2001	(TREMBrel. 16,	Created)	
DT 01-MAR-2001	(TREMBrel. 16,	Last sequence update)	
DT 01-JUN-2003	(TREMBrel. 24,	Last annotation update)	
DT Htr17 transducer.			
GN HTR17 OR VNG173G.			
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).			
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;			
OC Halobacteriaceae; Halobacterium.			
OX NCBI_TaxID=64091;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=20504483; PubMed=1116950;			
RA NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,			
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,			
RA Swartzell S., Weir D., Hall J., Dahl T.A., Dahl R., Goo Y.A.,			
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,			
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,			
RA Isenburger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,			
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,			
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;			
RT "Genome sequence of Halobacterium species NRC-1."			
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).			
DR EMBL; AE005078; AGI19368..1; -.			
DR PIR; DB4325; DB4325.			
DR HSSP; P02942; 1QUT7.			
DR GO; GO:0016020; C:membrane; IEA.			
DR GO; GO:0004811; F:signal transducer activity; IEA.			
DR GO; GO:0006335; P:chemotaxis; IEA.			
DR GO; GO:0007165; P:signal transduction; IEA.			
DR InterPro; IPR004089; Chmtaxis_transd.			
DR InterPro; IPR003660; HAMP.			
DR InterPro; IPR004090; Me_chemotaxis.			
DR PF00015; MCPsignat; 1.			
DR PRINTS; PRO00260; CHEMTRANSDFCR.			
DR SMART; SM00304; HAMP; 1.			
DR SMART; SM00283; MA; 1.			
DR PROSITE; PS50111; CHEMOTAXIS_TRANSduc_2; 1.			
DR PROSITE; PS500885; HAMP; 1.			
KW Complete proteome.			
SQ SEQUENCE 536 AA; 56815 MW; 3B33D2FDD8701EE04 CRC64;			
Query Match 100.0%; Score 34; DB 17; Length 536;			
Best Local Similarity 100.0%; Pred. No. 2.4e+02;			
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy 1 DGDGFA 6			
Db 358 DGDGFA 363			

Search completed: June 1, 2004, 18:09:54
Job time : 41 secs